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0.63

0.63

FILE 'MEDLINE' ENTERED AT 14:18:46 ON 29 APR 2004

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=> s myelogenous leukemia

L1 22800 MYELOGENOUS LEUKEMIA

=> s "HOIPS I"

L3 18 "HOIPS I"

=> s 13 and 12

L4 0 L3 AND L2

=> s 13 and 11

TI

L5 2 L3 AND L1

=> d 15 ti abs ibib tot

L5 ANSWER 1 OF 2 USPATFULL on STN

Human oncogene induced secreted protein I

The present invention relates to a novel protein, the Human Oncogene Induced Secreted Protein I ("HOIPS I") protein. In particular, isolated nucleic acid molecules are provided encoding the human HOIPS I protein. HOIPS I polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. Also provided are diagnostic methods for detecting abnormal cell proliferation and differentiation disorders and therapeutic methods for treating the same.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:

2002:221411 USPATFULL

TITLE:
INVENTOR(S):

Human oncogene induced secreted protein I Olsen, Henrik S., Gaithersburg, MD, UNITED STATES

Ruben, Steven M., Olney, MD, UNITED STATES

PATENT ASSIGNEE(S):

Human Genome Sciences, Inc. (U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 2002119552	A1	20020829	
APPLICATION INFO.:	US 2001-899917	A1	20010709	(9

RELATED APPLN. INFO.:

Division of Ser. No. US 1997-994962, filed on 19 Dec

1997, PATENTED

			NUMBER	DATE	
PRIORITY IN	FORMATION:	US	1996-33869P	19961220	(60)
			1997-37388P	19970207	(60)

DOCUMENT TYPE:

Utility

APPLICATION FILE SEGMENT:

STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C., 1100 NEW LEGAL REPRESENTATIVE:

YORK AVENUE, N.W., SUITE 600, WASHINGTON, DC,

20005-3934

NUMBER OF CLAIMS: 16 EXEMPLARY CLAIM:

NUMBER OF DRAWINGS: 4 Drawing Page(s)

2059 LINE COUNT:

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ANSWER 2 OF 2 USPATFULL on STN L5

ΤI Human oncogene induced secreted protein I

The present invention relates to a novel protein, the Human Oncogene AΒ Induced Secreted Protein I ("HOIPS I") protein. In particular, isolated nucleic acid molecules are provided encoding the human HOIPS I protein. HOIPS I

polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. Also provided are diagnostic methods for detecting abnormal cell proliferation and differentiation disorders and therapeutic methods for treating the same.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:

2001:147697 USPATFULL

TITLE:

Human oncogene induced secreted protein I

INVENTOR(S):

Olsen, Henrik S., Gaithersburg, MD, United States

Ruben, Steven M., Olney, MD, United States

PATENT ASSIGNEE(S):

Human Genome Sciences, Inc., Rockville, MD, United

States (U.S. corporation)

	NUMBER	KIND	DATE	
PATENT INFORMATION:	US 6284486	B1	20010904	
APPLICATION INFO.:	US 1997-994962		19971219	(8)
DOCUMENT TYPE:	Utility			
FILE SEGMENT:	GRANTED			
PRIMARY EXAMINER:	Carlson, Karen Co			
LEGAL REPRESENTATIVE:	Sterne, Kessler,	Goldste	ein & Fox	P.L.L.C.

LEGAL REPRESENTATIVE: NUMBER OF CLAIMS: 69

EXEMPLARY CLAIM: 1

NUMBER OF DRAWINGS:

4 Drawing Figure(s); 4 Drawing Page(s) LINE COUNT: 1994

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d his

L2

(FILE 'HOME' ENTERED AT 14:17:20 ON 29 APR 2004)

FILE 'MEDLINE, USPATFULL, DGENE, EMBASE, WPIDS, JICST-EPLUS' ENTERED AT 14:18:46 ON 29 APR 2004

22800 S MYELOGENOUS LEUKEMIA L1

142 S MYELOID CELL PROLIFERATION

18 S "HOIPS I" L3 0 S L3 AND L2 L41.5 2 S L3 AND L1

=> d 13 ti abs ibib tot

- ANSWER 1 OF 18 USPATFULL on STN L3
- Human oncogene induced secreted protein I ΤI
- The present invention relates to a novel protein, the Human Oncogene AΒ Induced Secreted Protein I ("HOIPS I") protein. In particular, isolated nucleic acid molecules are provided encoding the human HOIPS I protein. HOIPS I

polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. Also provided are diagnostic methods for detecting abnormal cell proliferation and differentiation disorders and therapeutic methods for treating the same.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:

2002:221411 USPATFULL

TITLE:

Human oncogene induced secreted protein I

INVENTOR(S):

Olsen, Henrik S., Gaithersburg, MD, UNITED STATES

Ruben, Steven M., Olney, MD, UNITED STATES

PATENT ASSIGNEE(S):

Human Genome Sciences, Inc. (U.S. corporation)

NUMBER KIND DATE ______ US 2002119552 A1 US 2001-899917 A1 20020829 PATENT INFORMATION: 20010709 APPLICATION INFO.:

RELATED APPLN. INFO.:

(9) Division of Ser. No. US 1997-994962, filed on 19 Dec

1997, PATENTED

NUMBER DATE _____

PRIORITY INFORMATION:

US 1996-33869P 19961220 (60) US 1997-37388P 19970207 (60)

DOCUMENT TYPE:

Utility

FILE SEGMENT:

APPLICATION

LEGAL REPRESENTATIVE:

STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C., 1100 NEW

YORK AVENUE, N.W., SUITE 600, WASHINGTON, DC,

20005-3934

NUMBER OF CLAIMS:

16 1

EXEMPLARY CLAIM: NUMBER OF DRAWINGS:

4 Drawing Page(s)

LINE COUNT:

2059

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ANSWER 2 OF 18 USPATFULL on STN L3

ΤI Human oncogene induced secreted protein I

The present invention relates to a novel protein, the Human Oncogene AB

Induced Secreted Protein I ("HOIPS I") protein. In

particular, isolated nucleic acid molecules are provided encoding the

human HOIPS I protein. HOIPS I

polypeptides are also provided as are vectors, host cells and recombinant methods for producing the same. Also provided are diagnostic methods for detecting abnormal cell proliferation and differentiation disorders and therapeutic methods for treating the same.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER:

2001:147697 USPATFULL

TITLE:

Human oncogene induced secreted protein I

INVENTOR (S):

Olsen, Henrik S., Gaithersburg, MD, United States

Ruben, Steven M., Olney, MD, United States

PATENT ASSIGNEE(S):

Human Genome Sciences, Inc., Rockville, MD, United

States (U.S. corporation)

NUMBER KIND DATE ______ US 6284486 B1 20010904 US 1997-994962 19971219 PATENT INFORMATION: 19971219 (8) APPLICATION INFO.: DOCUMENT TYPE: Utility

FILE SEGMENT: GRANTED
PRIMARY EXAMINER: Carlson, Karen Cochrane

LEGAL REPRESENTATIVE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

NUMBER OF CLAIMS:

69

EXEMPLARY CLAIM: NUMBER OF DRAWINGS:

4 Drawing Figure(s); 4 Drawing Page(s)

LINE COUNT: 1994

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L3 ANSWER 3 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAW69220 Protein DGENE

AB This sequence is the human oncogene induced secreted protein I (
HOIPS I) of the invention. HOIPS I

can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAW69220 Protein DGENE

TITLE: New isolated human oncogene induced secreted protein - used

to develop products for the diagnosis and treatment of cell

proliferative diseases, particularly cancers such as

leukaemia

INVENTOR: Olsen H S; Ruben S M

PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421 A1 19980702 71p

APPLICATION INFO: WO 1997-US23547 19971219 PRIORITY INFO: US 1997-37388 19970207

US 1996-33869 19961220

DOCUMENT TYPE: Patent LANGUAGE: English

OTHER SOURCE: 1998-377652 [32] CROSS REFERENCES: N-PSDB: AAV44745

DESCRIPTION: Human oncogene induced secreted protein I.

L3 ANSWER 4 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAV44751 cDNA DGENE

AB This sequence represents an expressed sequence tag, which is specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human oncogene induced secreted protein I (HOIPS I). HOIPS I can be used for

treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44751 cDNA DGENE

TITLE: New isolated human oncogene induced secreted protein - used

to develop products for the diagnosis and treatment of cell

71p

proliferative diseases, particularly cancers such as

leukaemia

INVENTOR: Olsen H S; Ruben S M

PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421 A1 19980702

APPLICATION INFO: WO 1997-US23547 19971219 PRIORITY INFO: US 1997-37388 19970207

US 1996-33869 19961220

DOCUMENT TYPE: Patent LANGUAGE: English

OTHER SOURCE: 1998-377652 [32]

DESCRIPTION: Expressed sequence tag C02431.

L3 ANSWER 5 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

ΑN AAV44750 cDNA **DGENE**

This sequence represents an expressed sequence tag, which is specifically AB stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human oncogene induced secreted protein I (HOIPS I) . HOIPS I can be used for

treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44750 cDNA DGENE

New isolated human oncogene induced secreted protein - used TITLE:

to develop products for the diagnosis and treatment of cell

proliferative diseases, particularly cancers such as

leukaemia

Olsen H S; Ruben S M **INVENTOR:**

PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.

PATENT INFO: A1 19980702 WO 9828421 71p

APPLICATION INFO: WO 1997-US23547 19971219 US 1997-37388 PRIORITY INFO: 19970207 US 1996-33869 19961220

DOCUMENT TYPE: Patent LANGUAGE: English

OTHER SOURCE: 1998-377652 [32]

DESCRIPTION: Expressed sequence tag T84854.

L3ANSWER 6 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

ΤI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AAV44749 cDNA DGENE ΑN

AB This sequence represents an expressed sequence tag, which is specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human oncogene induced secreted protein I (HOIPS I) . HOIPS I can be used for

treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44749 cDNA DGENE

New isolated human oncogene induced secreted protein - used TITLE:

to develop products for the diagnosis and treatment of cell

proliferative diseases, particularly cancers such as

leukaemia

Olsen H S; Ruben S M INVENTOR:

PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421 A1 19980702 71p

APPLICATION INFO: WO 1997-US23547 19971219 PRIORITY INFO: US 1997-37388 19970207

US 1996-33869 19961220

DOCUMENT TYPE: Patent LANGUAGE: English

OTHER SOURCE: 1998-377652 [32]

DESCRIPTION: Expressed sequence tag T92475.

T.3 ANSWER 7 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TТ New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN DGENE AAV44748 cDNA

This sequence represents an expressed sequence tag, which is specifically AB stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human oncogene induced secreted protein I (HOIPS I) . HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44748 cDNA DGENE

TITLE: New isolated human oncogene induced secreted protein - used

to develop products for the diagnosis and treatment of cell

proliferative diseases, particularly cancers such as

leukaemia

INVENTOR: Olsen H S; Ruben S M

PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421 A1 19980702 71p

APPLICATION INFO: WO 1997-US23547 19971219 PRIORITY INFO: US 1997-37388 19970207 US 1996-33869 19961220

DOCUMENT TYPE: Patent LANGUAGE: English

OTHER SOURCE: 1998-377652 [32]

DESCRIPTION: Expressed sequence tag T91708.

L3 ANSWER 8 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAV44758 DNA DGENE

AB This sequence is a PCR primer for DNA encoding the human oncogene induced secreted protein I (HOIPS I) of the invention.

HOIPS I can be used for treating cell proliferative

diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44758 DNA DGENE

TITLE: New isolated human oncogene induced secreted protein - used

to develop products for the diagnosis and treatment of cell

71p

proliferative diseases, particularly cancers such as

leukaemia

INVENTOR: Olsen H S; Ruben S M

PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421 A1 19980702

APPLICATION INFO: WO 1997-US23547 19971219
PRIORITY INFO: US 1997-37388 19970207

US 1996-33869 19961220

DOCUMENT TYPE: Patent LANGUAGE: English

OTHER SOURCE: 1998-377652 [32]

DESCRIPTION: Primer for Human oncogene induced secreted protein I.

L3 ANSWER 9 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAV44757 DNA DGENE

AB This sequence is a PCR primer for DNA encoding the human oncogene induced secreted protein I (HOIPS I) of the invention.

HOIPS I can be used for treating cell proliferative

diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44757 DNA DGENE

TITLE: New isolated human oncogene induced secreted protein - used

to develop products for the diagnosis and treatment of cell

proliferative diseases, particularly cancers such as

leukaemia

INVENTOR: Olsen H S; Ruben S M

PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421 A1 19980702 71p

APPLICATION INFO: WO 1997-US23547 19971219 PRIORITY INFO: US 1997-37388 19970207

US 1996-33869 19961220

DOCUMENT TYPE: I

Patent English

OTHER SOURCE:

1998-377652 [32]

DESCRIPTION:

Primer for Human oncogene induced secreted protein I.

L3 ANSWER 10 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAV44756 DNA DGENE

AB This sequence is a PCR primer for DNA encoding the human oncogene induced secreted protein I (HOIPS I) of the invention.

HOIPS I can be used for treating cell proliferative

diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44756 DNA DGENE

TITLE: New isolated human oncogene induced secreted protein - used

to develop products for the diagnosis and treatment of cell

71p

71p

proliferative diseases, particularly cancers such as

leukaemia

INVENTOR: Olsen H S; Ruben S M

PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421 A1 19980702

APPLICATION INFO: WO 1997-US23547 19971219

PRIORITY INFO: US 1997-37388 19970207

US 1996-33869 19961220

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: 1998-377652 [32]

DESCRIPTION: Primer for Human oncogene induced secreted protein I.

L3 ANSWER 11 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAV44755 DNA DGENE

AB This sequence is a PCR primer for DNA encoding the human oncogene induced secreted protein I (HOIPS I) of the invention.

HOIPS I can be used for treating cell proliferative

diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44755 DNA DGENE

TITLE: New isolated human oncogene induced secreted protein - used

to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as

profilerative diseases, particularly cant

19961220

leukaemia

INVENTOR: Olsen H S; Ruben S M

PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421 A1 19980702

APPLICATION INFO: WO 1997-US23547 19971219 PRIORITY INFO: US 1997-37388 19970207

US 1996-33869
DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: 1998-377652 [32]

DESCRIPTION: Primer for Human oncogene induced secreted protein I.

L3 ANSWER 12 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

New isolated human oncogene induced secreted protein - used to develop TI products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AAV44754 DNA DGENE AN

This sequence is a PCR primer for DNA encoding the human oncogene induced AB secreted protein I (HOIPS I) of the invention.

HOIPS I can be used for treating cell proliferative

diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44754 DNA DGENE

TITLE: New isolated human oncogene induced secreted protein - used

to develop products for the diagnosis and treatment of cell

proliferative diseases, particularly cancers such as

leukaemia

INVENTOR: Olsen H S; Ruben S M

PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421 A1 19980702 71p

APPLICATION INFO: WO 1997-US23547 19971219 US 1997-37388 PRIORITY INFO: 19970207 US 1996-33869 19961220

DOCUMENT TYPE: Patent LANGUAGE: English

OTHER SOURCE: 1998-377652 [32]

DESCRIPTION: Primer for Human oncogene induced secreted protein I.

ANSWER 13 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN L3

New isolated human oncogene induced secreted protein - used to develop TI products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

ΔN AAV44753 DNA DGENE

AB This sequence is a PCR primer for DNA encoding the human oncogene induced secreted protein I (HOIPS I) of the invention.

HOIPS I can be used for treating cell proliferative

diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44753 DNA DGENE

TITLE: New isolated human oncogene induced secreted protein - used

to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as

leukaemia

INVENTOR: Olsen H S; Ruben S M

PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421 A1 19980702 71p

APPLICATION INFO: WO 1997-US23547 19971219 PRIORITY INFO: US 1997-37388 19970207 US 1996-33869 19961220

DOCUMENT TYPE: Patent

LANGUAGE: English

OTHER SOURCE: 1998-377652 [32]

DESCRIPTION: Primer for Human oncogene induced secreted protein I.

ANSWER 14 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT On STN L3

TTNew isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAV44752 DNA DGENE

This sequence is a PCR primer for DNA encoding the human oncogene induced AB secreted protein I (HOIPS I) of the invention.

HOIPS I can be used for treating cell proliferative

diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44752 DNA DGENE

TITLE: New isolated human oncogene induced secreted protein - used

to develop products for the diagnosis and treatment of cell

71p

71p

proliferative diseases, particularly cancers such as

leukaemia

INVENTOR: Olsen H S; Ruben S M

PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421 A1 19980702

APPLICATION INFO: WO 1997-US23547 19971219 PRIORITY INFO: US 1997-37388 19970207

US 1996-33869 19961220

DOCUMENT TYPE: Patent LANGUAGE: English

OTHER SOURCE: 1998-377652 [32]

DESCRIPTION: Primer for Human oncogene induced secreted protein I.

L3 ANSWER 15 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAV44746 cDNA DGENE

AB This sequence represents an expressed sequence tag, which is specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human oncogene induced secreted protein I (HOIPS I). HOIPS I can be used for

treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44746 cDNA DGENE

TITLE: New isolated

New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell

proliferative diseases, particularly cancers such as

leukaemia

INVENTOR: Olsen H S; Ruben S M

PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.

PATENT ASSIGNEE: (HOMA-N/HOMAN GENOME SCI INC. PATENT INFO: WO 9828421 A1 19980702

APPLICATION INFO: WO 1997-US23547 19971219

PRIORITY INFO: US 1997-37388 19970207 US 1996-33869 19961220

DOCUMENT TYPE: Patent

LANGUAGE: English
OTHER SOURCE: 1998-377652 [32]

DESCRIPTION: Expressed sequence tag.

L3 ANSWER 16 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

TI New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AN AAV44747 CDNA DGENE

AB This sequence represents an expressed sequence tag, which is specifically stated as not being contained within the DNA of the invention. The DNA of the invention encodes the human oncogene induced secreted protein I (HOIPS I). HOIPS I can be used for

treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44747 cDNA DGENE

TITLE: New isolated human oncogene induced secreted protein - used

to develop products for the diagnosis and treatment of cell

proliferative diseases, particularly cancers such as

leukaemia

INVENTOR: Olsen H S; Ruben S M

(HUMA-N) HUMAN GENOME SCI INC. PATENT ASSIGNEE:

A1 19980702 WO 9828421 PATENT INFO: APPLICATION INFO: WO 1997-US23547 19971219

US 1997-37388 19970207 PRIORITY INFO: US 1996-33869 19961220

DOCUMENT TYPE:

Patent

LANGUAGE:

English

OTHER SOURCE:

1998-377652 [32]

DESCRIPTION:

Expressed sequence tag AA340310.

ANSWER 17 OF 18 DGENE COPYRIGHT 2004 THOMSON DERWENT on STN

DGENE

New isolated human oncogene induced secreted protein - used to develop TIproducts for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia

AAV44745 cDNA AN

This sequence encodes the human oncogene induced secreted protein I (AB HOIPS I) of the invention. HOIPS I

can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of a cell proliferative or cell differentiation disorders.

ACCESSION NUMBER: AAV44745 cDNA DGENE

TITLE:

New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell

71p

71p

proliferative diseases, particularly cancers such as

leukaemia

INVENTOR:

Olsen H S; Ruben S M

PATENT ASSIGNEE: (HUMA-N) HUMAN GENOME SCI INC.

PATENT INFO: WO 9828421

A1 19980702

PRIORITY INFO:

APPLICATION INFO: WO 1997-US23547 19971219 US 1997-37388 19970207

US 1996-33869 19961220

DOCUMENT TYPE:

Patent

LANGUAGE:

English

OTHER SOURCE:

1998-377652 [32]

CROSS REFERENCES: P-PSDB: AAW69220

DESCRIPTION:

Human oncogene induced secreted protein I coding sequence.

- ANSWER 18 OF 18 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN L3
- New isolated human oncogene induced secreted protein used to develop TIproducts for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia.
- AN 1998-377652 [32] WPIDS
- 9828421 A UPAB: 19980812 AΒ

An isolated nucleic acid molecule (I) is claimed comprising a polynucleotide (PN) having a nucleotide sequence (NS) at least 95% identical to a sequence selected from:

- (a) a NS encoding a polypeptide comprising amino acids from -20 to 142, -19 to 142, or 1 to 142 of the 162 amino acid (aa) sequence given in the specification (sequence representing a Human Oncogene Induced Secreted Protein I (HOIPS I) polypeptide);
- (b) a NS encoding a polypeptide having an amino acid sequence encoded by a cDNA clone contained in ATCC 97825;
- (c) a NS encoding a mature HOIPS I polypeptide having an amino acid sequence encoded by a cDNA clone contained in ATCC 97825; and
 - (d) a NS complementary to any of the NSs in (a)-(c). Also claimed are:
- (1) an isolated Nucleic Acid Molecule (NAM) comprising a PN which hybridises under stringent hybridisation conditions (I) where the PN which hybridises does not hybridise under stringent hybridisation conditions to a PN having a NS consisting of only A residues or of only T residues;
- (2) an isolated NAM comprising a PN which encodes an amino acid sequence of an epitope-bearing portion of a HOIPS I

polypeptide having an amino acid sequence as in (a)-(c) above;

- (3) an isolated NAM comprising a PN having a sequence at least 95% identical to a sequence selected from:
- (a) a NS of a fragment of a 860 bp sequence given in the specification (encoding the HOIPS I polypeptide), where the fragment comprises at least 50 contiguous nucleotides of the 860 bp, provided that the NS is not one of the 514, 457, 413, 320, 264, and 249 sequences given in the specification; and
 - (b) a NS complementary to a NS as in (a);
- (4) a method for making a recombinant vector comprising inserting (I) into a vector;
 - (5) a recombinant vector produced by a method as in (4);
- (6) a method of making a recombinant host cell comprising introducing a recombinant vector as in (5) into a host cell;
 - (7) a recombinant host cell produced by a method as in (6);
 - (8) an isolated HOIPS I polypeptide having an

amino acid sequence at least 95% identical to a sequence encoded by (I) or an epitope-bearing portion of the polypeptide;

- (9) an isolated polypeptide comprising an epitope-bearing portion of the HOIPS I protein, where the portion is selected from a polypeptide comprising amino acid residues from -4 to 9, from 13 to 19, from 23 to 32, from 36 to 47, from 54 to 63, from 70 to 74, from 90 to 100, from 105 to 119 or from 125 to 132 of the 162 aa sequence;
- (10) an isolated **HOIPS I** polypeptide where, except for 1 to 50 conservative amino acid substitutions, the polypeptide has a sequence selected from:
- (a) amino acids from -20 to 142, 19 to 142, or 1 to 142 of the 162 aa sequence given in the specification;
- (b) an amino acid sequence of the HOIPS I polypeptide having an amino acid sequence encoded by a cDNA contained in ATCC 97825;
- (c) an amino acid sequence of a mature HOIPS I polypeptide having an amino acid sequence encoded by a cDNA clone contained in ATCC 97825; and
- (d) an amino acid sequence of an epitope-bearing portion of any one of the polypeptides as in (a)-(c);
 - (11) an isolated nucleic acid encoding a polypeptide as in (10).
- USE The products can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis. Dwg.0/3

ACCESSION NUMBER: 1998-377652 [32] WPIDS

DOC. NO. NON-CPI: N1998-295209 DOC. NO. CPI: C1998-114764

TITLE: New isolated human oncogene induced secreted protein used to develop products for the diagnosis and treatment
of cell proliferative diseases, particularly cancers such

as leukaemia.

DERWENT CLASS: B04 D16 S03

INVENTOR(S): OLSEN, H S; RUBEN, S M

PATENT ASSIGNEE(S): (HUMA-N) HUMAN GENOME SCI INC

COUNTRY COUNT: 8

PATENT INFORMATION:

PATENT NO KIND DATE WEEK LA PO

WO 9828421 A1 19980702 (199832) * EN 71

RW: AT BE CH DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW

W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM GW HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW

AU 9858027 A 19980717 (199848)

US 6284486 B1 20010904 (200154) US 2002119552 A1 20020829 (200259)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9828421 AU 9858027 US 6284486	A1 A B1 Provisional Provisional	WO 1997-US23547 AU 1998-58027 US 1996-33869P US 1997-37388P	19971219 19971219 19961220 19970207
US 2002119552	Al Provisional Provisional Div ex	US 1997-994962 US 1996-33869P US 1997-37388P US 1997-994962 US 2001-899917	19971219 19961220 19970207 19971219 20010709

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 9858027	A Based on	WO 9828421

PRIORITY APPLN. INFO: US 1997-37388P

19970207; US 19961220; US 1996-33869P 19971219; US 1997-994962 20010709 2001-899917

Refine Search

Search Results -

Terms	Documents		
L9 and L10	18		

US Pre-Grant Publication Full-Text Database

US Patents Full-Text Database
US OCR Full-Text Database
EPO Abstracts Database
JPO Abstracts Database
Derwent World Patents Index
IBM Technical Disclosure Bulletins

L11

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DATE: Thursday, April 29, 2004 Printable Copy Create Case

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<u>L11</u>	19 and L10	18	<u>L11</u>		
<u>L10</u>	ruben.in.	1520	<u>L10</u>		
<u>L9</u>	16 and L8	31	<u>L9</u>		
<u>L8</u>	olsen.in.	2539	<u>L8</u>		
<u>L7</u>	henrik-olsen.in.	0	<u>L7</u>		
<u>L6</u>	myelogenous leukemia and L5	10350	<u>L6</u>		
<u>L5</u>	myeloid proliferation and 14	29144	<u>L5</u>		
<u>L4</u>	L3 and protein sequence	614907	<u>L4</u>		
<u>L3</u>	human oncogene induced secreted protein I	1403401	<u>L3</u>		
<u>L2</u>	HOIPs-I	0	<u>L2</u>		
<u>L1</u>	6284486.pn.	1	<u>L1</u>		

END OF SEARCH HISTORY

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Search Results - Record(s) 1 through 10 of 18 returned.

☐ 1. Document ID: US 6632920 B1

L11: Entry 1 of 18

File: USPT

Oct 14, 2003

US-PAT-NO: 6632920

DOCUMENT-IDENTIFIER: US 6632920 B1

TITLE: 36 human secreted proteins

DATE-ISSUED: October 14, 2003

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY Olsen; Henrik S. Gaithersburg MDRuben; Steven M. MD Olney Rosen; Craig A. Laytonsville MD Brewer; Laurie A. St. Paul MN Ebner; Reinhard Gaithersburg MD Bethesda Duan; Roxanne MD Florence; Kimberly Rockville MD

US-CL-CURRENT: 530/300; 435/69.1, 530/324

Full Titl	e Citation	Front	Review	Classification	Date	Reference	esperie Macha	ustrias i Cila	ims K	MC	Draw, D
П 2.	Docume	nt ID:	US 66	27741 B2	1420,000 (144 market of 144 market of 14						

US-PAT-NO: 6627741

DOCUMENT-IDENTIFIER: US 6627741 B2

TITLE: Antibodies to secreted protein HCEJQ69

DATE-ISSUED: September 30, 2003

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Ruben; Steven M. Olney MD

Ni; Jian Germantown MD

h eb bgeeef e ef be

Rosen; Craig A.	Laytonsville	MD
Wei; Ying-Fei	Berkeley	CA
Young; Paul	Gaithersburg	MD
Florence; Kimberly	Rockville	MD
Soppet; Daniel R.	Centreville	VA
Brewer; Laurie A.	St. Paul	MN
Endress; Gregory A.	Florence	MA
Carter; Kenneth C.	North Potomac	MD
Mucenski; Michael	Cincinnati	ОН
Ebner; Reinhard	Gaithersburg	MD
LaFleur; David W.	Washington	DC
Olsen; Henrik	Gaithersburg	MD
Shi; Yanggu	Gaithersburg	MD
Moore; Paul A.	Germantown	MD
Komatsoulis; George	Silver Spring	MD

US-CL-CURRENT: <u>530/389.2</u>; <u>530/387.1</u>, <u>530/387.3</u>, <u>530/387.7</u>, <u>530/387.9</u>, <u>530/388.1</u>, <u>530/388.15</u>, <u>530/389.1</u>

Full Ti	tle Citation	Front Review	Classification	Date Referen	se sullishme	Alta Apple	Claims	KWAC	: Dramu (
								,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	
□ 3.	Documen	nt ID: US 60	505592 B2						
L11: En	try 3 of 3	18		File:	USPT		Aug	12,	2003

US-PAT-NO: 6605592

DOCUMENT-IDENTIFIER: US 6605592 B2

TITLE: Protein HOFNF53

DATE-ISSUED: August 12, 2003

INVENTOR-INFORMATION:

INVENTOR INCOMBILION.					
NAME	CITY	STATE	ZIP	CODE	COUNTRY
Ni; Jian	Germantown	MD			
Baker; Kevin P.	Darnestown	MD			
Birse; Charles E.	North Potomac	MD			
Ebner; Reinhard	Gaithersburg	MD			
Fiscella; Michele	Bethesda	MD			
Komatsoulis; George A.	Silver Spring	MD			
LaFleur; David W.	Washington	DC			
Moore; Paul A.	Germantown	MD			
Olsen; Henrik S.	Gaithersburg	MD			
Rosen; Craig A.	Laytonsville	MD			
Ruben; Steven M.	Olney	MD			
Soppet; Daniel R.	Centreville	VA			
Young; Paul E.	Gaithersburg	MD			
Wei; Ping	Brookeville	MD			

h e b b g e e e f b

Florence; Kimberly A. Rockville

MD

US-CL-CURRENT: 514/2; 435/252.3, 435/254.11, 435/320.1, 435/325, 435/471, 435/69.1, <u>435/71.1</u>, <u>435/71.2</u>, <u>514/12</u>, <u>514/8</u>, <u>530/350</u>

Full Title Citation F	ront Review Classificatio	n Date Reference	Sequences Attachments	Claims	KWIC	Draw, De
☐ 4. Document	ID: US 6590075 B2			Alless union a libroreos una	-1-11/2	
L11: Entry 4 of 18	3	File:	USPT	Jul	8,	2003

US-PAT-NO: 6590075

DOCUMENT-IDENTIFIER: US 6590075 B2

TITLE: Secreted protein HODAZ50

DATE-ISSUED: July 8, 2003

INVENTOR-INFORMATION:

L11: Entry 5 of 18

NAME	CITY	STATE	ZIP CODE	COUNTRY
Ruben; Steven M.	Olney	MD		
Rosen; Craig A.	Laytonsville	MD		
Fischer; Carrie L.	Burke	AV		
Soppet; Daniel R.	Centreville	VA		
Carter; Kenneth C.	North Potomac	MD		
Bednarik; Daniel P.	Columbia	MD		
Endress; Gregory A.	Potomac	MD		
Yu; Guo-Liang	Berkeley	CA		
Ni; Jian	Rockville	MD		
Feng; Ping	Gaithersburg	MD		
Young; Paul E.	Gaithersburg	MD		
Greene; John M.	Gaithersburg	MD		
Ferrie; Ann M.	Tewksbury	MA		
Duan; Roxanne	Bethesda	MD		
Hu; Jing-Shan	Sunnyvale	CA		
Florence; Kimberly A.	Rockville	MD		
Olsen; Henrik S.	Gaithersburg	MD		
Ebner; Reinhard	Gaithersburg	MD		
Brewer; Laurie A.	St. Paul	MN		
Shi; Yanggu	Gaithersburg	MD		

US-CL-CURRENT: 530/350; 435/6, 435/69.1, 435/7.1, 536/23.1

Full	Title	e Citation Front	Review Classification	Date	Reference	Sellerises	Eliaciments	Claims	KWIC	Draw, D
,	5.	Document ID:	US 6576445 B1							

File: USPT

Jun 10, 2003

ef b e eb b g ee e f

US-PAT-NO: 6576445

DOCUMENT-IDENTIFIER: US 6576445 B1

TITLE: Chemokine .alpha.-4

DATE-ISSUED: June 10, 2003

INVENTOR-INFORMATION:

ZIP CODE COUNTRY STATE NAME CITY

Gaithersburg MD Olsen; Henrik S. MDOlney Ruben; Steven M. Gaithersburg MD Zeng; Zhi-Zhen

 $\text{US-CL-CURRENT:} \ \underline{435/69.5}; \ \underline{435/325}, \ \underline{530/300}, \ \underline{530/350}, \ \underline{530/386}, \ \underline{530/387.1}, \ \underline{530/387.3},$ 530/387.9, 530/388.1, 530/388.15, 530/388.23, 530/389.1, 530/389.2, 530/391.1, 530/391.3, 530/391.5, 530/391.7, 530/391.9

Full	Title	Citation	Front	Review	Classification	Date	Reference	The Market State of S	Claims	KMAC	Drawi D
							!				

6. Document ID: US 6566325 B2

L11: Entry 6 of 18

File: USPT May 20, 2003

US-PAT-NO: 6566325

DOCUMENT-IDENTIFIER: US 6566325 B2

TITLE: 49 human secreted proteins

DATE-ISSUED: May 20, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Moore; Paul A.	Germantown	MD		
Ruben; Steven M.	Olney	MD		
Olsen; Henrik S.	Gaithersburg	MD		
Shi; Yanggu	Gaithersburg	MD		
Rosen; Craig A.	Laytonsville	MD		
Florence; Kimberly A.	Rockville	MD		
Soppet; Daniel R.	Centreville	VA		
LaFleur; David W.	Washington	DC		
Endress; Gregory A.	Potomac	MD		
Ebner; Reinhard	Gaithersburg	MD		
Komatsoulis; George	Silver Spring	MD		
Duan; Roxanne D.	Bethesda	MD		

US-CL-CURRENT: 514/2; 530/300, 530/350

Full Title Citation Front Review Classification Date Reference Seculation Stackments Claims KWI	Drawu
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7. Document ID: US 6548063 B1

L11: Entry 7 of 18

File: USPT

MD

Apr 15, 2003

US-PAT-NO: 6548063

DOCUMENT-IDENTIFIER: US 6548063 B1

TITLE: Synferon

DATE-ISSUED: April 15, 2003

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Olsen; Henrik S. Gaithersburg

Gentz; Reiner L. Rockville MD

Ruben; Steven M. Olney MD

US-CL-CURRENT: 424/158.1; 424/85.4, 435/325, 530/350, 530/351, 530/388.1, 530/389.1

Full Title Citation Front Review Classification Date Reference Stripe Ses Attachnierts Claims KWIC Draw. Ds

8. Document ID: US 6534631 B1

L11: Entry 8 of 18 File: USPT Mar 18, 2003

US-PAT-NO: 6534631

DOCUMENT-IDENTIFIER: US 6534631 B1

TITLE: Secreted protein HT5GJ57

DATE-ISSUED: March 18, 2003

INVENTOR-INFORMATION:

CITY STATE ZIP CODE COUNTRY NAME Ruben; Steven M. MD Olney Komatsoulis; George Silver Spring MD Duan; Roxanne D. Bethesda MD Rosen; Craig A. Laytonsville MD Moore; Paul A. Germantown MD Gaithersburg MD Shi; Yanggu LaFleur; David W. Washington DC Ebner; Reinhard Gaithersburg MD Olsen; Henrik Gaithersburg MD Brewer; Laurie A. St. Paul MN Florence; Kimberly A. Rockville MD Young; Paul Gaithersburg MD Cincinnati Mucenski; Michael OH Endress; Gregory A. Potomac MD Soppet; Daniel R. Centreville VA

h e b b g e e e f b e

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US-CL-CURRENT: $\underline{530}/\underline{350}$; $\underline{435}/\underline{320.1}$, $\underline{435}/\underline{325}$, $\underline{530}/\underline{300}$, $\underline{536}/\underline{23.1}$, $\underline{536}/\underline{24.1}$

Full Title Citation Front Review Classific	ation Date Reference Saguences 7	Atachinents Claims KMC Draw De
☐ 9. Document ID: US 6525174	B1	
L11: Entry 9 of 18	File: USPT	Feb 25, 2003

US-PAT-NO: 6525174

DOCUMENT-IDENTIFIER: US 6525174 B1

TITLE: Precerebellin-like protein

DATE-ISSUED: February 25, 2003

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP	CODE	COUNTRY
Young; Paul	Gaithersburg	MD			
Greene; John M.	Gaithersburg	MD			
Ferrie; Ann M.	Tewksbury	MA			
Ruben; Steven M.	Olney	MD			
Rosen; Craig A.	Laytonsville	MD			
Hu; Jing-Shan	Sunnyvale	CA			
Olsen; Henrik S.	Gaithersburg	MD			
Ebner; Reinhard	Gaithersburg	MD			
Brewer; Laurie A.	St. Paul	MN			
Moore; Paul A.	Germantown	MD			
Shi; Yanggu	Gaithersburg	MD			
Florence; Charles	Rockville	MD			
Florence; Kimberly	Rockville	MD			
Lafleur; David W.	Washington	DC			
Ni; Jian	Rockville	MD			
Fan; Ping	Gaithersburg	MD			
Wei; Ying-Fei	Berkeley	CA			
Fischer; Carrie L.	Burke	VA			
Soppet; Daniel R.	Centreville	VA			
Li; Yi	Sunnyvale	CA			
Zeng; Zhizhen	Gaithersburg	MD			
Kyaw; Hla	Frederick	MD			
Yu; Guo-Liang	Berkeley	CA			
Feng; Ping	Gaithersburg	MD			
Dillon; Patrick J.	Carlsbad	CA			
Endress; Gregory A.	Potomac	MD			
Carter; Kenneth C.	North Potomac	MD			
Carter, Renneth C.	NOT CIT FOCOMIAC	MD			

US-CL-CURRENT: <u>530/350</u>; <u>435/69.1</u>

Full	Title	Citation	Front	Review	Classification	Date	Reference	Serverno ac-	(Alterdamental)	Claims	KWIC	Draw De

□ 10. Document ID: US 6476195 B1

L11: Entry 10 of 18

File: USPT

Nov 5, 2002

US-PAT-NO: 6476195

DOCUMENT-IDENTIFIER: US 6476195 B1

TITLE: Secreted protein HNFGF20

DATE-ISSUED: November 5, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Komatsoulis; George	Silver Spring	MD		
Rosen; Craig A.	Laytonsville	MD		
Ruben; Steven M.	Olney	MD		
Duan; Roxanne D.	Bethesda	MD		
Moore; Paul A.	Germantown	MD		
Shi; Yanggu	Gaithersburg	MD		
LaFleur; David W.	Washington	DC		
Wei; Ying-Fei	Berkeley	CA		
Ni; Jian	Rockville	MD		
Florence; Kimberly A.	Rockville	MD		
Young; Paul	Gaithersburg	MD		
Brewer; Laurie A.	St. Paul	MN		
Soppet; Daniel R.	Centreville	AV		
Endress; Gregory A.	Potomac	MD		
Ebner; Reinhard	Gaithersburg	MD		
Olsen; Henrik	Gaithersburg	MD		
Mucenski; Michael	Cincinnati	ОН		

US-CL-CURRENT: 530/350; 435/6, 435/7.1, 536/23.1

Full	Title Citation Front Review Class	sification Date Reference Sequences Altochin	episk Claims KWC Draw.
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☐ 11. Document ID: US 6475753 B1

L11: Entry 11 of 18

File: USPT

Nov 5, 2002

US-PAT-NO: 6475753

DOCUMENT-IDENTIFIER: US 6475753 B1

TITLE: 94 Human Secreted Proteins

DATE-ISSUED: November 5, 2002

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY MD Ruben; Steven M. Olney Ni; Jian Rockville MD Laytonsville Rosen; Craig A. MD Berkeley CA Wei; Ying-Fei Gaithersburg MD Young; Paul Rockville MD Florence; Kimberly Centreville Soppet; Daniel R. VA Brewer; Laurie A. St. Paul MN Endress; Gregory A. Potomac MD Carter; Kenneth C. Potomac MD Mucenski; Michael Cincinnati OH Ebner; Reinhard Gaithersburg MD Lafleur; David W. Washington DC MD Olsen; Henrik Gaithersburg Gaithersburg MD Shi; Yanggu Moore; Paul A. Germantown MD Silver Spring Komatsoulis; George MD

US-CL-CURRENT: 435/69.1; 435/252.3, 435/320.1, 435/325, 435/471, 435/69.4, 435/71.1, 530/350, 536/23.5

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences Attachments	Claims	KMC	Draw, De

☐ 12. Document ID: US 6433139 B1

L11: Entry 12 of 18

File: USPT

Aug 13, 2002

Jul 16, 2002

US-PAT-NO: 6433139

DOCUMENT-IDENTIFIER: US 6433139 B1

TITLE: Secreted protein HPEAD48

DATE-ISSUED: August 13, 2002

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Ruben; Steven M. Olney MD
Rosen; Craig A. Laytonsville MD
Olsen; Henrik S. Gaithersburg MD

US-CL-CURRENT: $\underline{530}/\underline{350}$; $\underline{435}/\underline{6}$, $\underline{435}/\underline{7.1}$, $\underline{530}/\underline{300}$, $\underline{536}/\underline{23.1}$

Full	Title	Citation	Front	Review	Classification	Date Refere	nce (*) com	- Alterbrieds	Claims	KMIC	Draim, D
									***		<u></u>
	13	Docum	ent IF) US 6	420526 B1						

File: USPT

US-PAT-NO: 6420526

L11: Entry 13 of 18

DOCUMENT-IDENTIFIER: US 6420526 B1

TITLE: 186 human secreted proteins

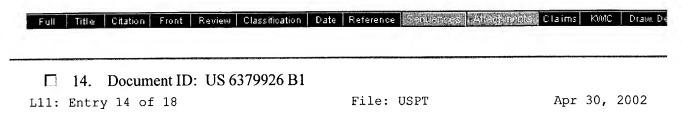
DATE-ISSUED: July 16, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP	CODE	COUNTRY
Ruben; Steven M.	Olney	MD			
Rosen; Craig A.	Laytonsville	MD			
Fischer; Carrie L.	Burke	VA			
Soppet; Daniel P.	Centreville	VA			
Carter; Kenneth C.	North Potomac	MD			
Bednarik; Daniel R.	Columbia	MD			
Endress; Gregory A.	Potomac	MD			
Yu; Guo-Liang	Berkeley	CA			
Ni; Jian	Rockville	MD			
Feng; Ping	Gaithersburg	MD			
Young; Paul E.	Gaithersburg	MD			
Greene; John M.	Gaithersburg	MD			
Ferrie; Ann M.	Tewksbury	MA			
Duan; Roxanne	Bethesda	MD			
Hu; Jing-Shan	Sunnyvale	CA			
Florence; Kimberly A.	Rockville	MD			
Olsen; Henrik S.	Gaithersburg	MD			
Ebner; Reinhard	Gaithersburg	MD			
Brewer; Laurie A.	St. Paul	MN			

Germantown MD Moore; Paul A. MD Gaithersburg Shi; Yanggu DC Lafleur; David W. Washington Sunnyvale CA Li; Yi Lansdale PA Zeng; Zhizhen Frederick MD Kyaw; Hla

US-CL-CURRENT: 530/350; 435/6, 536/23.1



US-PAT-NO: 6379926

DOCUMENT-IDENTIFIER: US 6379926 B1

TITLE: Polynucleotides encoding chemokine .beta.-6 antagonists

DATE-ISSUED: April 30, 2002

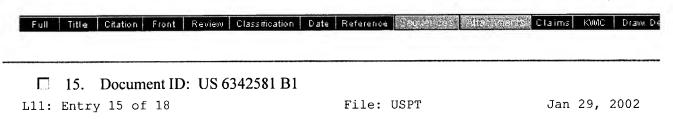
INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Kreider; Brent L. Germantown MD
Ruben; Steven M. Olney MD
Olsen; Henrik S. Gaithersburg MD

US-CL-CURRENT: 435/69.5; 435/252.3, 435/320.1, 435/325, 435/455, 435/471, 435/69.1,

<u>435/69.7</u>, <u>536/23.1</u>, <u>536/23.4</u>, <u>536/23.5</u>



US-PAT-NO: 6342581

DOCUMENT-IDENTIFIER: US 6342581 B1

** See image for Certificate of Correction **

TITLE: Secreted protein HLHFP03

DATE-ISSUED: January 29, 2002

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Rosen; Craig A. Laytonsville MD Ruben; Steven M. Olney MD

Olsen; Henrik S.

Gaithersburg

MD

Ebner; Reinhard

Gaithersburg

MD

US-CL-CURRENT: 530/300; 435/69.1, 530/350

Full Title Citation Front Review Classification Date Reference Acquairdes Attachipents Claims KMC Draw De

☐ 16. Document ID: US 6284486 B1

L11: Entry 16 of 18

File: USPT

Sep 4, 2001

US-PAT-NO: 6284486

DOCUMENT-IDENTIFIER: US 6284486 B1

TITLE: Human oncogene induced secreted protein I

DATE-ISSUED: September 4, 2001

INVENTOR-INFORMATION:

NAME CI'

CITY

STATE

ZIP CODE C

COUNTRY

Olsen; Henrik S.

Gaithersburg

MD

Ruben; Steven M.

Olney

MD

US-CL-CURRENT: 435/69.1; 435/252.3, 435/6, 435/91.1, 435/91.4, 435/91.41, 536/23.1, 536/23.5, 536/24.1, 536/24.2

Full Title Citation Front Review Classification Date Reference Couldings Altochnicities Claims KWIC Draw De

L11: Entry 17 of 18

File: USPT

Sep 5, 2000

US-PAT-NO: 6114145

DOCUMENT-IDENTIFIER: US 6114145 A

TITLE: Synferon, a synthetic interferon

☐ 17. Document ID: US 6114145 A

DATE-ISSUED: September 5, 2000

INVENTOR-INFORMATION:

NAME CI'

CITY

STATE ZIP CODE

COUNTRY

Olsen; Henrik S.

Gaithersburg

MD

COONTRI

Gentz; Reiner L.

Rockville

MD

Ruben; Steven M.

Olney

MD

US-CL-CURRENT: 435/69.51; 424/85.4, 435/252.3, 435/252.33, 435/254.11, 435/325, 435/455, 435/471, 435/91.41, 530/351, 536/23.52

Full Title Citation Front Review Classification Date Reference (Superiors) Altachments Claims KMC Draw De

☐ 18. Document ID: US 5916769 A

L11: Entry 18 of 18

File: USPT

Jun 29, 1999

US-PAT-NO: 5916769

DOCUMENT-IDENTIFIER: US 5916769 A

TITLE: Polynucleotides encoding extra cellular/epidermal growth factor HCABA58X

polypepides

DATE-ISSUED: June 29, 1999

INVENTOR-INFORMATION:

NAME

CITY

STATE

ZIP CODE

COUNTRY

Olsen; Henrik S.

Gaithersburg

MD

Ruben; Steven M.

Olney

MD

US-CL-CURRENT: 435/69.4; 435/243, 435/320.1, 435/325, 435/69.1, 536/23.1, 536/23.51

Full -	Title Citation Front R	eview Class	ification	Date	Reference	7		n i	Claims	KWMC	Dravu De
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
	862	100.0	162	» į	AAW69220	Aaw69220 Human onc
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10	613		162	7	ADE59272	Ade59272 Rat Prote
11	336		160	w	AAY77482	Aay77482 Avian pro
12	336		160	6	ABU61847	1847
13	106		160	N	AAY13929	
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Abm70549	Aao19184	Abb92360	Abp65007	Aab95041	Abp63008	Abp63009	Adc64335	Aar29640	Aay32057	Abb91291	Aab56960	Ade38437	Adb75603	Aay32037	Abu24033	Aag30766	Aag30767	Aag30768	Abu26566
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ALIGNMENTS

AAW69220 standard; protein; 162 AA.

16-OCT-1998 (first entry)

Human oncogene induced secreted protein I.

Oncogene induced secreted protein I; HOIPS I; human; cancer; therapy; cell proliferative disease; myelogenous leukaemia; cell differentiation disorder.

Homo sapiens.

Protein Peptide Location/Qualifiers /note= "signal peptide" note= "mature HOIPS I" .162

W09828421-A1

02-JUL-1998.

19-DEC-1997; 97WO-US023547.

20-DEC-1996; 07-FEB-1997; 96US-0033869P. 97US-0037388P.

(HUMA-) HUMAN GENOME SCI INC.

Olsen HS, Ruben SM;

N-PSDB; AAV44745. WPI; 1998-377652/32.

New isolated human oncogene induced secreted protein - used to develop products for the diagnosis and treatment of cell proliferative diseases, particularly cancers such as leukaemia.

Claim 12; Page 51-52; 71pp; English.

This sequence is the human oncogene induced secreted protein I (HOIPS I) of the invention. HOIPS I can be used for treating cell proliferative diseases, particularly cancers, such as acute and chronic myelogenous leukaemias. The products can also be used for detection and diagnosis of

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                                                                    This sequence represents a OHP106 protein of the invention. The polypoptides and their antibodies are applicable in drug compositions, useful for treatment of various diseases including bacterial and viral infections with cytokine activity, and activities e.g. on cell proliferation/differentiation, immunostimulation/suppression, control haemacopoiesis, and tissue formation and repair. The proteins and antibodies have a wide spectrum of activities
                                                                                                                                                                                                                                                                                                                                                                                                                                    OHP106; bacterial; viral; infection; cytokine activity; tissue formation; cell proliferation; cell differentiation; immunostimulation; therapy; immunosuppression; haematopoiesis control; tissue repair.
                                                Sequence 162
                                                                                                                                                                  Claim 1; Page 47; 57pp; Japanese.
                                                                                                                                                                                        New polypeptides useful in the treatment of various diseases including bacterial and viral infections with cytokine activity.
                                                                                                                                                                                                                                           WPI; 1999-277269/23
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The invention discloses a composition comprising two or more isolated rat cor human polynucleotides or a polynucleotide which represents a fragment, constraint or a rectangle of the nucleic acid sequence. Also comprising the vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a comprising the vector, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal cubjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal compound that regulates the activity of one or more of the polynucleotides of a polynucleotide sequence which is differentially compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a pharmaceutical composition, a period for identifying a compound useful in treating specification, a method for identifying a compound useful in treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction conjury (CCI) and spared nerve injury (Chung), chronic constriction conjury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene theres). The sequence presented is a human protein (shown in Table 2 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Protein 095711,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page; 1017pp;
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segmental nerve injury; chronic constriction injury; CCI;
nerve injury; SNI; Chung.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUL-1998;
13-JUL-1998;
23-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-AUG-1998;
18-AUG-1998;
11-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MD-1; MD-2; leucine-rich motif; LRR protein ligand; immune inflammation; allergy; immunosuppressant; antiarthritic; an antiinflammatory; dermatological; antithyroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
The invention relates to a number of primate and/or rodent proteins, and the genes which encode them. The invention encompasses human dendritic cell prostaglandin transporter (DC-PGT); the TNF (tumour necrosis factor) receptor family-related proteins HDTEAS4, HSLJD37R and RANKL; human CC chemokine HCCS; human deubiquitinating proteins Dub11 and Dub 12; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-1999;
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                                                                                                                                                                                                                                                  New isolated mammalian genes, used to develop products for treating e.g. immune, inflammatory or allergic abnormalities, cancers or degenerative
                                                                                                                                                                                                                                                                                                                                     WPI; 2000-171015/15.
N-PSDB; AAZ92417.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLKSNINIRFGIILREDIKELFLDLALMSQGSSVLNFSYPICEAALPKFSFCGRRKGEQI 120
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                                                                                                                                                                                                                                                                                                                                                                                                            Lebecque SJE, Murphy EE, Mattson JD, Gorman
A, Wang L, Zlotnik A, Murgolo NJ, Greene JR,
Mahony D, Lees EM;
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98US-00114466.
98US-0093897P.
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98US-0099999P.
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Pred. No. 9e-92;
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                                                                                           Matches
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Best Local :
                                                                                                                                                                                                                                              interactions (e.g., induce or prevent trafficking, proliferation, or differentiation of cells), or are intracellular proteins which are important in various cellular processes such as the deubiquitination of proteins or cell cycle regulation. The products can be used for treating medical conditions such as immune, inflammatory or allergic disorders, o abnormal cellular proliferation, for example, cancers or degenerative conditions. They can be used to modulate immune responses in disease e.g., autoimmune disorders, including rheumatoid arthritis, as wel systemic lupus crythematosus, Hashimoto's autoimmune thyroiditis, as wel as acute and chronic inflammatory responses in which T cell activation, expansion, and/or immunological T cell memory play an important role. Sequences AAY77476-Y77478 are human MD-2 proteins. AAY77479 is murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MD-1 and human and murine MD-2 proteins, which exhibit the properties of ligands for proteins comprising a leucine-rich motif (LRR); human cyclin E2; cDNAs encoding these proteins; and antibodies against these proteins. The proteins can be used for modulating the physiology or development of a cell. They can be used to mediate uptake of substrates (e.g., prostaglandin-like molecules), to modulate or mediate cellular interactions (a.g., induce or modulate or mediate cellular interactions).
                                                                                                                                                                                      Sequence 162
                                                                                           161;
                                                                                                                   Similarity
  MKGFTATLFLWTLIFPSCSGGGGKAMPTHVVCSDSRLEVLYQSCDPLQDFGFSVEKCSK
                                              MKGFTATLFLWTLIFPSCSGGGGGKAWPTHVVCSDSGLEVLYQSCDPLQDFGFSVEKCSK
                                                                                                                                                                                                                                  AAY77480
                                                                                           Conservative
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                                                                                                                                                                                                                               primate MD-2
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                                                                                                                 Score 854; DB 3; Pred. No. 7.7e-91;
                                                                                             Mismatches
                                                                                                                                       Length 162;
                                                                                             Indels
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121
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                             YYAGPVNNPEFTIPQGEYQVLLELYTEKRSTVACANATIMCS 162
                                                                                                                   QLKSNINIRFGIILREDIKELFLDLALMSQGSSVLNFSYPICEAALPKFSFCGRRKGEQI 120
YYAGPVNNPEFTIPQGEYQVLLELYTEKRSTVACANATIMCS
                                                                                 OLKSNINIRFGIILREDIKELFLDLALMSQGSSVLNFSYPICEAALPKFSFCGRRKGEQI
  162
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RESULT 5
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ABUG6
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XX ABUG
XX ABUG
XX Huma
XX Huma
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"Encoded
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11-AUG-1999;

12-AUG-1998; (BAZA/) BAZAN

> 98US-0096328P 99US-00372348

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Misc-difference

/note= 37

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/label= Unknown /note= "Encoded

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RESULT 6
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Best Local S
Matches 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New composition comprising HCC5, Dubl1, Dubl2, primate MD1 or MD2 or rodent MD2 polypeptide, useful for modulating physiology or developm of a cell or tissue culture cells.
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N-PSDB; ACA62461.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 162
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                                              autoimmune
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                                         new DNA encoding a utoimmune diseases,
                                                                                                          2000-353476/31.
DB; AAA11221.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>QLKSNINIRFGIILREDIKELFLDLALMSQGSSVLNFSYPICEAALPKFSFCGRRKGEQI</u>
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20. .162
/note= "mature |
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                                                                                                                                                                                   CORP
                                              B cell surface protein, gic diseases, asthma and
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Claim

1:

Page 11;

12pp; Japanese

This sequence represents a OHP106 protein of the invention. The polypeptides and their antibodies are applicable in drug compose useful for treatment of various diseases including bacterial are infections with cytokine activity, and activities e.g. on cell proliferation/differentiation, immunostimulation/suppression, charactopoiesis, and tissue formation and repair. The proteins a harmatopoiesis, and tissue formation and repair.

compositions,

and viral control

O.F

antibodies have a wide spectrum of

activities

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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a human B cell surface protein, designated MD-1 The protein is involved in the inhibition or induction of B cell apoptosis and has antiallergic, antiasthmatic, immunosuppressive, dermatological and antiinflammatory activity. The protein and the DNA and used as treating and diagnostic agents for diseases related to antibody production by B cells, e.g. autoimmune or allergic diseases, asthma and atopic dermatitis. The coding sequence was isolated from a human EST clone (GenBank accession number T84854)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OHP106; bacterial; viral; infection; cytokine activity; tissue cell proliferation; cell differentiation; immunostimulation; th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 162
                                                                                                                                                                                                                                                                   New polypeptides useful in the treatment bacterial and viral infections with cytol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-APR-1999.
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DB; AAX36693, AJ
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                                                                                                                                                                                                                                                                                                                                                                                                                       Kato K,
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88.9%;
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Pred. No. 1.1e-79;
3; Mismatches 15
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13-JUL-1998;
23-JUL-1998;
12-AUG-1998;
18-AUG-1998;
11-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bates EEM,
Hedrick JA,
The invention relates to a number of primate and/or rodent proteins, and the genes which encode them. The invention encompasses human dendritic cell prostaglandin transporter (DC-PGT); the TNF (tumour necrosis factor) receptor family-related proteins HDTEA84, HSLJD378 and RANKI; human CC chemokine HCC5; human deubiquitinating proteins Dubl1 and Dub 12; human MD-1 and human and murine MD-2 proteins, which exhibit the properties of ligands for proteins comprising a leucine-rich motif (LRR); human cyclin E2; cDNAs encoding these proteins; and antibodies against these proteins. The proteins can be used for modulating the physiology or development of a cell. They can be used for modulating the physiology or development of prostaglandin-like molecules), to modulate or mediate cellular prostaglandin-like molecules), to modulate or mediate cellular interactions (e.g., induce or prevent trafficking, proliferation, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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antirheumatoid;
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                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 208-209; 218pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mahony D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lebecque SJE, Murphy
Wang L, Zlotnik A,
Mahony D, Lees EM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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98US-00114466.
98US-0093897P.
98US-00132968.
98US-00136214.
98US-0099999P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammation; allergy; immunosuppressant; antiarthritic; antiinflammatory; dermatological; antithyroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.1%; Score 613; 66.7%; Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID NO:50.
                                                                                                                                                                                                                                                                                                                                                                                                                   ed to develop products for abnormalities, cancers or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murgolo NJ, Greene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; L
3.5e-63;
nes 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 162
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ene JR,
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                                                                                                                                                                                                                                                                                                                                                                                                                      treating e.g
degenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Johnston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          important in various cellular processes such as the deubiquitination of proteins or cell cycle regulation. The products can be used for treating medical conditions such as immune, inflammatory or allergic disorders, or abnormal cellular proliferation, for example, cancers or degenerative conditions. They can be used to modulate immune responses in disease states e.g., autoimmune disorders, including rheumatoid arthritis, systemic lupus exythematosus, Hashimoto's autoimmune thyroiditis, as well as acute and chronic inflammatory responses in which T cell activation, as acute and chronic inflammatory responses in which T cell activation, capansion, and/or immunological T cell memory play an important role. Cequences Ax171463-Y77464, Ax777474-Y77475 and Ax777484 represent primate proteins of undefined function, Ax777482 and Ax777481 are rodent proteins of undefined function, Ax777482 and Ax777481 are rodent proteins of function. These sequences are given in the sequence listing but are not creferred to in the remainder of the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Sim
Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       differentiation of cells),
                                                                                                                                                                           Bazan JF;
                                                                                                                                                                                                                                                          11-AUG-1999;
                                                                                                                                                                                                                                                                                      06-FEB-2003.
                                                                                                                                                                                                                                                                                                                US2003028005-A1
                                                                                                                                                                                                                                                                                                                                          Mus sp.
                                                                                                                                                                                                                                                                                                                                                                   Mouse; MD1;
                                                                                                                                                                                                                                                                                                                                                                                                Mouse MD1
                                                                                                                                                                                                                                                                                                                                                                                                                          15-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU61846;
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                                                                                                                                                                                                                                  12-AUG-1998;
                                                                                                                                                                                                   (BAZA/) BAZAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YYAGPVNNPEFTIPQGEYQVLLELYTEKRSTVACANATIMCS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QIQSNLNIRFGIILRQDIRKLFLDITLMAKGSSILNYSYPLCEEDQPKFSFCGRRKGEQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
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                                                                                                                                                                                                                                                                                                                                                                      cell development; tissue
                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                  98US-0096328P
                                                                                                                                                                                                                                                             99US-00372348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; 162
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                                                                                                                                                                                                                                                                                                                                                                                                                          entry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 613; DB 3;
Pred. No. 8.5e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                       culture development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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orders, or
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The invention relates to a novel chemokine, de-ubiquitination surface protein. The composition is useful for modulating phys development of a cell or tissue culture cells. The present sec represents the amino acid sequence of mouse MD1

physiology or

or

New composition comprising HCC5, Dub11, Dub12, primate MD1 or rodent MD2 polypeptide, useful for modulating physiology or de of a cell or tissue culture cells.

development

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Disclosure;

Page 18; 77pp; English.

WPI;

2003-466159/44.

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ARESULT 10
ARDES9272
ID S0272
ID ADES9
XX ADES9
XX ADES9
XX ADES9
XX Rat;
KW Rat;
KW Chror
XX WC200
PM WC200
XX Rattu
XX MC200
PM WC200
PM 14-Au
XX MC200
PM 01-WC
PR 26-WC
XX MC200
PM CGEH
PA (FARE
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Best Local Similarity 66.7%;
Matches 108; Conservative 22
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claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound that regulates the activity of one or more of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-2002; 2002WO-US025765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rat Protein NP_034875,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                           The invention discloses a composition comprising two or more isolated or human polynucleotides or a polynucleotide which represents a fragme derivative or allelic variation of the nucleic acid sequence. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New composition comprising preparing a medicament for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-268312/26.
GENBANK; NP_034875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEHO )
(FARB )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page; 1017pp; English
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BAYER AG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                two or more isolated polypeptides, useful treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy; spinal segmental nerve injury;
; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162
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Pred. No. 8.5e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Costigan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                               fragment,
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                                                                                                                                                                                                                                                                                                                                                                                                             rat
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WPI; 2000-171015/15. N-PSDB; AAZ92421.

New isolated mammalian genes, used immune, inflammatory or allergic ak

ed to develop products for treating e.g. abnormalities, cancers or degenerative

inflammatory

immune, in conditions

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RESULT 11
AAY77482
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Best Local
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                                                                                                                                                                                       23-JUL-1998;
12-AUG-1998;
18-AUG-1998;
11-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                  Imune disorder;
antirheumatoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 162 AA;
                                                                                                                                                                                                                                            06-JUL-1998;
13-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                        Aves
                                                                                                                                                                                                                                                                                                                                                                                                                                           Avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY77482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY77482 standard; protein; 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
                                                                                                      Bates EEM, Lebecque SJE, Murphy EE, Mattson JD, Gc
Hedrick JA, Wang L, Zlotnik A, Murgolo NJ, Greene
Bazan JF, Mahony D, Lees EM;
                                                                                                                                                                                                                                                                                        06-JUL-1999;
                                                                                                                                                                                                                                                                                                                 13-JAN-2000
                                                                                                                                                                                                                                                                                                                                             WO200001817-A2
                                                                                                                                                              (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 QLKSNINIRFGIILREDIKELFLDLALMSQGSSVLNFSYPICEAALPKFSFCGRRKGEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YYAGPVNNPGLDVPQGEYQLLLELYNENRATVACANATVTSS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QIQSNLNIRFGIILRQDIRKLFLDITLMAKGSSILNYSYPLCEEDQPKFSFCGRRKGEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MNGVAAALLVWILTSPSSSDHGSENGWPKHTACNSGGLEVVYQSCDPLQDFGLSIDQCSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MKGFTATLFLWTLIFPSCSGGGGKAWPTHVVCSDSGLEVLYQSCDPLQDFGFSVEKCSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YYAGPVNNPEFTIPQGEYQVLLELYTEKRSTVACANATIMCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence, SEQ ID
                                                                                                                                                                                         98US-00132968.
98US-00136214.
98US-00999999.
                                                                                                                                                                                                                                  98US-00114466.
98US-0093897P.
                                                                                                                                                                                                                                                              98US-00110938
                                                                                                                                                                                                                                                                                        99WO-US012366
                                                                                                                                                                                                                                                                                                                                                                                                 inflammation; allergy; immunosuppressant; antiarthritic; antiinflammatory; dermatological; antithyroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 613; DB 7;
Pred. No. 8.5e-63;
2; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                           NO:52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162
                                                                                                                                       Gorman
                                                                                                                          JR,
                                                                                                                                       DM.
                                                                                                                            Johnston
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Disclosure; Page 210-211; 218pp; English

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CC the genes which encode them. The invention encompasses human dendritic cell prostenglandin transporter (DC-PGT); the TNF (tumour necrosis factor) creceptor family-related proteins HDTEA84, HSLJD37R and RANKL; human CC chemokine HGC5; human deubiquitinating proteins Dubil and Dub 12; human CC CC chemokine HGC5; human deubiquitinating proteins Dubil and Dub 12; human CC CC ligands for proteins comprising a leucine-rich motif (LRR); human cyclin CC ligands for proteins comprising a leucine-rich motif (LRR); human cyclin CC acll. They can be used for modulating the physiology or development of CC a cell. They can be used to mediate uptake of substrates (e.g., or compositions), or are intracellular proteins which are important in various cellular processes such as the deubiquitination of CC abnormal cellular processes such as the deubiquitination of CC abnormal conditions such as immune, inflammatory or allergic disorders, or conditions. They can be used to modulate immune responses in disease states e.g., autoimmune disorders, including rhematoid arthritis, as well cas acute and chronic inflammatory responses in which T cell activation, cexpansion, and/or immunological T cell memory play an important role.

CC sequences AAY77465-Y77464, AAY77462 and AAY77481 are rodent proteins
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Best Local S
Matches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins of undefined function, AAY77462 and AAY77481 are rodent proteins of undefined function, and AAY77482 is an avian protein of undefined function. These sequences are given in the sequence listing but are not referred to in the remainder of the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 160 AA;
                                                                                                                                                                                         Gallus gallus.
                                                                                                                                                                                                                            Chicken; MD1; cell
                                                                                                                                                                                                                                                                 Chicken
                                                                                                                                                                                                                                                                                                    15-AUG-2003
                                                                                                                                                                                                                                                                                                                                          ABU61847
                                                                                                                                                                                                                                                                                                                                                                        ABU61847 standard; protein; 160 AA
                                                   12-AUG-1998;
                                                                                   11-AUG-1999;
                                                                                                                                                         US2003028005-A1
             (BAZA/) BAZAN J F
                                                                                                                                                                                                                                                                                                                                                                                                                                                               142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 WPTHVVCSDSGLEVLYQSCDPLQDFGFSVEKCSKQLKSNINIRFGIILREDIKELFLDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKRSTVACANATI 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WETHTVCKEENLEIYYKSCDPQQDFAFSIDRCSDVTTHTFDIRAAMVLRQSIKELYAKVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDRATVACADETV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIINGKTVLSYSETLCGPGLSKLIFCGKKKGEHLYYEGPITLGIKEIPORDYTITARLTN 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LWSQGSSVINESYPICEAALPKESECGRRKGEQIYYAGPVNNPEETIPQGEYQVILLELYT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          relates to
                                                   98US-0096328P
                                                                                     99US-00372348
                                                                                                                                                                                                                             development; tissue culture development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.0%; Score 336; DB 3; Length 160; 44.4%; Pred. No. 1.4e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a number of primate and/or rodent proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel chemokine, de-ubiquitination or cesurface protein. The composition is useful for modulating physiological phy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New composition comprising HCC5, Dub11, Dub12, primate MD1 or MD2 or rodent MD2 polypeptide, useful for modulating physiology or developm of a cell or tissue culture cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-466159/44.
N-PSDB; ACA62465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OHP106; bacterial; viral; infection; cytokine activity; tissue format cell proliferation; cell differentiation; immunostimulation; therapy; immunosuppression; haematopoiesis control; tissue repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 160
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                                                                         Claim 1;
                                                                                                                       New polypeptides useful in the treatment of various diseases including bacterial and viral infections with cytokine activity.
                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                WPI; 1999-277269/23.
                                                                                                                                                                                                                                                                              Honjo T,
                                                                                                                                                                                                                                                                                                                                                                                07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                 06-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9918205-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse OHP106 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-APR-1999.
                                                                                                                                                                                                                                                                                                                                  (ONOY ) ONO PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142
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                                                                                                                                                                                                   AAX36687, AAX36688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKRSTVACANATI 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPTHTVCKEENLEIYYKSCDPQQDFAFSIDRCSDVTTHTFDIRAAMVLRQSIKELYAKVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPTHVVCSDSGLEVLYQSCDPLQDFGFSVEKCSKQLKSNINIRFGIILREDIKELFLDLA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDRATVACADETY 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIINGKTVLSYSETLCGPGLSKLIFCGKKKGEHLYYEGPITLGIKEIPORDYTITARLTN 141
                                                                         Page 36-37; 57pp; Japanese.
                                                                                                                                                                                                                                                                              Kato K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΑA;
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                                                                                                                                                                                                                                                                                                                                                                                     97JP-00274673
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                                                                                                                                                                                                                                                                              Tada H;
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44.4%; Pred. No. 1.46
tive 26; Mismatches
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This sequence represents a OHP106 protein of the invention. The polypeptides and their antibodies are applicable in drug compositions.

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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A new protein controlling the infection-preventing microbe.
                                                                                                                                                                                                                                    has immunosuppressant, antiallergy; antiastimatic and dermatological activity. The protein and the DNA can be used as a treating agent and a diagnostic agent for diseases such as autoimmune diseases, allergic diseases, asthma and atopic dermatitis
                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a protein, MD-2, which controls an infection prevention reaction against a microbe. Protein and cDNA sequences AAC66387 - AAB35928 represent human and mouse I 2. MD-2 increases NFKappaB activation through TLP4 molecules. The protein and control of the protein against the protein 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
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    Score 106; DB 3;
Pred. No. 0.00084;
P4; Mismatches 61
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Pred. No. 0.00084;
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RESULT 15
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proliferation; cell differentiation;
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   GSKGLLHIFYIPRRDIKQLYFNLYITVNTMNLPKRKEVICRGSDDDYSFCRALKGETVNT 115
                                                   KSNINIRFGIILREDIKELFLDLALMSQGSSVLNFSYPICEAALPKFSFCGRRKGEQIYY 122
                                                                                                                                                                     FTATLFLWTLIFPSCSGGGGGKAWPTHVVCSDSGLEVLYQSCDPLQ-DFGFSVEKCSKQL 62
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Pred. No. 0.0028;
26; Mismatches 70;
                                                                                                               -EAQKQYWVCNSSDASISYTYCDKMQYPISINVNPCIELK
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116 TISFSFKGIKFSKGKYKCVVE 136

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Search completed: April 29, 2004, 15:22:20 Job time : 60 secs

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Perfect score:
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seq length: 2000000000
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363.626 Million cell updates/sec
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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                                                                                                                                                                                                                                                                                          Copyright
                                                                        GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-09-252-991A-26468

5470718-2

US-08-530-950-13

US-09-149-879-13

US-09-149-879-13

US-09-281-385C-4

US-09-285-385C-4

US-09-285-391A-27242

US-09-285-991A-27242

US-08-336-618-26

US-08-336-618-26

US-08-136-618-26

US-08-136-618-26

US-08-36-618-26

US-08-36-618-26

US-08-36-618-26

US-08-36-618-26

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US-08-36-618-26

US-08-36-618-28

US-08-564-805-227
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US-08-994-962-3

US-08-969-644-16

US-08-969-644-16

US-08-444-189-16

US-08-444-189-16

US-08-468-544-16

US-08-260-151-22

US-08-413-118-22

US-08-413-118-22
                                                                sequence 3, Appli sequence 16, Appl sequence 16, Appl sequence 16, Appl sequence 22, Appl sequence 22, Appl sequence 22, Appl sequence 22, Appl sequence 24, Appl sequence 26468, A Patent No. 5470718 Sequence 13, Appl sequence 13, Appl sequence 13, Appl sequence 12, Appl sequence 12, Appl sequence 12, Appl sequence 27, Appl sequence 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                        ; MOLECULE TYPE:
US-08-994-962-2
     Query Match
Best Local Similarity
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ALIGNMENTS	US-09-845-583A-2	US-09-108-020-16	US-09-134-000C-6022	US-09-323-998E-60	US-09-201-641-2	US-09-911-842A-5	5472939-2	5256642-2	5472939-10	5256642-10	US-08-030-096-8	US-09-491-577-4	US-09-198-452A-155	5	US-08-569-853-2	9-853-	05-2	US-08-676-444-5	
	Sequence 2, Appli	Sequence 16, Appl	602	60,	2, Appl	Sequence 5, Appli	Patent No. 5472939	Patent No. 5256642	Patent No. 5472939	٠	Sequence 8, Appli	Sequence 4, Appli	Sequence 155, App	Sequence 1, Appli	Sequence 2, Appli	Sequence 1, Appli	e 12	Sequence 5, Appli	

RESULT 1

(Scylence 2, Application US/08994962)

Patent No. 6284486

Patent No. 6284486

GENERAL INFORMATION:

APPLICANT: Ruben, Steven M.

TITLE De INVENTION:

APPLICANT: Ruben, Steven M.

TITLE De INVENTION:

APPLICANT: Ruben, Steven M.

TITLE De INVENTION:

APPLICANT: Olsen, Human Oncogene Induced Secreted Protein I

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler Goldstein & Fox P.L.L.C.

STREET: 1100 New York Ave., NW, Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Flopy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Flopy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Flopy disk

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MEDIUM TYPE: ON BATA:

APPLICATION NUMBER: US/08/94,962

FILING DATE: Herewith

CLASSIFICATION:

APPLICATION NUMBER: US 60/033,869

FILING DATE: 20-DEC-1996

CLASSIFICATION NUMBER: US 60/033,869

FILING DATE: 07-FEB-1997

CLASSIFICATION NUMBER: US 60/037,388

FRICH APPLICATION NUMBER: US 60/037,388

FRICH APPLICATION NUMBER: US 60/037,388

FRICH APPLICATION NUMBER: 1488.0440002

TELEPAX: 20-2371-2540

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 162 amino acids

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: protein

SOB-94-962-2

100.0%;

Score 862; DB 3; Pred. No. 8e-100;

Length 162

Mismatches

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Indels

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Gaps

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                                                                                                                Matches
                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: Herewith CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/033,869 FILING DATE: 20-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Olsen, Henrik S. APPLICANT: Ruben, Steven M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/037,388
FILING DATE: 07-FEB-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Human Oncogene Induced Secreted Protein
                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 110
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ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                 Local
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       87 LMSQGSSVLNFSYPICEAALPKFSFCGRRKGEQIYYAGPVNNPEFTIPQGEYQVLLELYT 146
                                                                                                              h 39.9%; Score 344; DB 3; Length 133; Similarity 45.1%; Pred. No. 4.2e-35; 60; Conservative 26; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MKGFTATLFLWTLIFPSCSGGGGKAWPTHVVCSDSGLEVLYQSCDPLQDFGFSVEKCSK 60
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                                        WPTHTVCKEENLEIYYKSCDPQQDFAFSIDRCSDVTTHTFDIRAAMVLRQSIKELYAKVD 60
                                                                           WPTHVVCSDSGLEVLYQSCDPLQDFGFSVEKCSKQLKSNINIRFGIILREDIKELFLDLA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Sterne, Kessler Goldstein & Fox P.L.L.C.
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not relevant
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RESULT 3
US-08-994-962-17
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                                                                                                                                                                                Query Match 10.9%;
Best Local Similarity 33.3%;
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Olsen, Henrik S.
APPLICANT: Ruben, Steven M.
                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGAIN.

NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488
REJECOMMUNICATION INFORMATION:
TELECOMMUNICATION 17024012600
                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 202-371-260
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/994,96:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FR PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/037,388
FILING DATE: 07-FEB-1997
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APPLICATION NUMBER: US 60/033,869
FILING DATE: 20-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Human Oncogene Induced Secreted Protein I NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1100 New CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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STREET: 1100 New York Ave.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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     147 EKRSTVACA 155
                                                                       87 LMSQGSSVLNFSYPICEAALPKFSFCGRRKGEQIYYAGPVNNPEFTIPQGEYQVLLELYT 146
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                                                                                                            WPTHV-----CLEYSCDP-QDF-FS---CSIRLR-----
                                                                                                                                         WPTHYVCSDSGLEVLYQSCDPLQDFGFSVEKCSKQLKSNINIRFGIILREDIKELFLDLA 86
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                                          -GVLSCLKFCG--KGE---YYGP----
                                                                                                                                                                                Score 94; DB 3;
Pred. No. 0.00027;
3; Mismatches 13
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                                                                                                                                                                                     13;
                                                                                                                                                                                                                      Length 60
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US-08-969-644-16
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Patent No. 6070---
Patent INFORMATION:
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                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
ATTORNEY AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 1267
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241_1300
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                 TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linco
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/969,644
FILING DATE: 13-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/467,152
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: BIRCH, STEWART, STREET: 301 N. Washington CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 703_241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/661,820 FILING DATE: IT MI 91A00031 FILING DATE: 07-FEB-1991
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ZIP: 22046-0747
100 HRGPSNN 106
                                 122 YAGPVNN 128
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                                                                                                 67 NIRFGIILREDIKELFLDLALMSQGSSVLNFSYPIÇEAA----LPKFSFCGRRKGEQIY 121
                                                                                                                                                                      10 LWTLIFPSCSGGGGGKAWPTHVVCSDS---GLEVLYQSCDFLQDFGFSVEKCSKQLKSNI 66
                                                                                                                                                                                                           35;
                                                                   SSGLGASVRSDQKGLH-DIVYTSNDLKSI----ICETKKDSVDLIPASFSSEQFRELDI 99
                                                                                                                                          LHTLVFCSFKGGTGKTTLSLNVGCNLAQFLGKKVLLADLDP
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TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED BY
THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
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Street
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Pred. No. 0.83;
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                                                                                                                                                                                                                                               DB 3;
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RESULT 5 US-08-444-189-16

> RESULT 6 US-08-468-544-16 ; Sequence 16, Application US/08468544

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APPLICANT: Ratti,
                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                               TELEX: 248345
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 264 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: IT M
FILING DATE: 07-FEB-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                   122 YAGPVNN 128
100
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                                                                                                        67 NIRFGIILREDIKELFLDLALMSQGSSVLNFSYPICEAA-----LPKFSFCGRRKGEQIY 121
                                                                                                                                                                             10 LWILLEPSCSGGGGKAWPTHYVÇSDS---GLEVLYQSCDPLQDFGFSVEKCSKQLKSNI 66
                                                                                                                                                                                                                   ch 8.5%; Score 73.5; DB 3; Length 264; l Similarity 27.6%; Pred. No. 0.83; 35; Conservative 13; Mismatches 50; Indels 2
                                                                                                                                              1 LHTLVFCSFKGGTGKTTLSLNVGCNLAQFLGKKVLLADLDF-----
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                                                                       SSGLGASVRSDQKGLH-DIVYTSNDLKSI---
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HRGPSNN
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TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED
THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
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                                                                           - icetkkosvolipasėsseofreldi 99
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US-08-220-151-22
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                                                                                                                                                                                                                                                  RESULT 7
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Matches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/468,544
FILING DATE: 06-JUN-1995
CLASSIFICATION 94
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/661,820
FILING DATE: 28-FEB-1991
APPLICATION NUMBER: IT MI 91A000314
FILING DATE: 07-FEB-1991
APPLICATION NUMBER: 07-FEB-1991
APPLICATION NUMBER: US 07/661,820
FILING DATE: 07-FEB-1991
APPLICATION SUMBER: US 07/661,820
APPLICATION NUMBER: US 07/661,820
FILING DATE: 07-FEB-1991
APPLICATION SUMBER: US 07/661,820
                                                                                                       Patent No. 5529780 GENERAL INFORMATION:
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TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 amino acid
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TITLE OF INVENTION: PCTD PLASMID ISOLATED FROM CHLAMYDIA
TITLE OF INVENTION: TRACHOMATIS SEROTYPE D, ITS GENES AND PROTEINS ENCODED
TITLE OF INVENTION: THEM; RECOMBINANT PLASMIDS FOR THE EXPRESSION OF SAID
TITLE OF INVENTION: GENES IN HETEROLOGOUS SYSTEMS, PREPARATION OF SAID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 30,330
REFRENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
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ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 301 N. Washington Street
CITY: Falls Church
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   TITLE OF INVENTION:
                              APPLICANT:
APPLICANT:
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 LWTLIFPSCSGGGGGKAWPTHVVCSDS---GLEVLYQSCDPLQDFGFSVEKCSKQLKSNI 66
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Similarity 27.6%; Pred. No. 0.83;
35; Conservative 13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LHTLVFCSFKGGTGKTTLSLNVGCNLAQFLGKKVLLADLDP
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                                                                                                                                              Application US/08220151
529780
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                              Paoletti,
Limbach, 1
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NUCLEOTIDE AND AMINO ACID SEQUENCES
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; FRAGMENT TYPE: N-terminal
US-08-220-151-22
                                                                                                                                                                                                                                                                                                                                                                    US-08-413-118-22
                                                                                                                                                                                                                                                                                                          Sequence 22, Applicat Patent No. 5688920 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Tocal Similarity
Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212) 840-0712
TELEX: 425066 CURTMS
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Frommer, William S. REGISTRATION NUMBER: 25,506 REFERENCE/DOCKET NUMBER: 45.506 REFERENCE/DOCKET NUMBER: 45.506 REFERENCE/DOCKET NUMBER: 45.506 REFERENCE/DOCKET NETELECOMMUNICATION INFORMATION: TELECOMMUNICATION 1040-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: CANINE HERPESVIRUS GB, NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS;
ADDRESSEE: Qurtis, Morris & Safford
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0
FILING DATE: 30-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS
STREET: 530 FIFTH AVENUE,
                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                          APPLICANT: PAOLETTI, ENZO
APPLICANT: LIMBACH, KEITH J.
TITLE OF INVENTION: UCCLEOTIDE AND AMINO ACID SEQUENCES OF
TITLE OF INVENTION: CANINE HERPESVIRUS GB, GC, AND GD AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                ZIP:
                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
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                                                                                                   NEW YORK
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                                                                   10036
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                                                                                                                                                                                                                                                                                                                                                 Application US/08413118
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                                                                                  UNITED STATES OF AMBRICA
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                                                                                                                                              MORRIS & SAFFORD,
AVENUE, 25TH FLOOR
                                                                                                                                                                                                         128
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Pred. No. 1.7;
17; Mismatches
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Matches
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REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2670
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-333
TELEPHONE: (212) 840-333
INFORMATION FOR SEQ ID NO: 22:
              FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 0/
PILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NOTHER: US/08/473,446
APPLICATION NUMBER: US/08/473,446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide FRAGMENT TYPE: N-terminal
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/413,118
FILING DATE: 29-MAR-1995
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
STREET: 530 FIFTH AVENUE, 25TH FLOOR
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                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 KTYSÄRL-TWFKIMPTC------ATPIH------DVSYMKCNPKLSFAMCDE----- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 LKSNINIRFGII--LREDIKELFLDLALMSQGSSVL------NFSYPICEAA 105
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amino acid
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                                                                                                                                                                                                                                                                             UNITED STATES
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NUCLEOTIDE AND AMINO ACID SEQUENCES
CANINE HERPESVIRUS 9B, 9C, AND 9D AN
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                                      08/413,118
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AND GD AND USES
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; FRAGMENT TYPE: N-terminal
US-08-473-446-22
                                                       RESULT 11
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                                     US-09-252-991A-26468
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APPLICANT: O'CALLAGHAN, DENNIS J.

TITLE OF INVENTION: EQUINE HERPESVIRUS TYPE 1 GLYCOPROTEIN

D NUCLEIC ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO:3:
Sequence 26468, Application US/09252991A Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45.
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/954,417
FILING DATE: 30-SEP-1992
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                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 01-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 LP----KFSFCGRRKGEQIYYAGPVNN----PEFTIPQGEYQVLLELY 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 KTYSARL-TWFKIMPTC-----ATPIH------DVSYMKCNPKLSFAMCDE------199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 -RSDÍLWQASLÍTMAAETDDELGLVLAAPAHSASGLYRRVIEIDGRRIYTDFSVTÍPSER 258
                                                                                                            259 CPIAFELNFGNPDRCKTPEQYSRGEVFTRRFLGEFNFPQGEHMTWVKFW 307
                                                                                                                                                106 LP----KFSFCGRRKGEQIYYAGPVNN----PEFTIPQGEYQVLLELY 145
                                                                                                                                                                                                                                                               161 KTYSARL-TWFKIMPTC----ATPIH-----DVSYMKCNPKLSFAMCDE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 LKSNINIRFGII--LREDIKELFLDLALMSQGSSVL-----NFSYPICEAA 105
                                                                                                                                                                                                                         62 LKSNINIRFGII--LREDIKELFLDLALMSQGSSVL------NFSYPICEAA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 8.5%; Score 73.5; D
1 Similarity 25.4%; Pred. No. 1.7;
43; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KGFTATLFLWTLIFPSCSGGGGKAWPTHVVCSDSGLEVLYQSCDPLQDFGFSVEKCSKQ 61
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                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CPIAFELNEGNEDRCKTPEQYSRGEVETRRELGEENEPQGEHMTWVKFW 307
                                                                                                                                                                                        -RSDÍLWQASLÍTMAAETDDÉLGLVLÁAPAHSASGLYRRVIEIDGRRIYTDÉSVTÍPSER 258
                                                                                                                                                                                                                                                                                                KGFTATLFLWTLIFPSCSGGGGKAWPTHVVCSDSGLEVLYQSCDPLQDFGFSVEKCSKQ 61
                                                                                                                                                                                                                                                                                                                                      Conservative
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linear
                                                                                                                                                                                                                                                                                                                                                    8.5%; Score 73.5; DB 6; 25.4%; Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    561,553
                                                                                                                                                                                                                                                                                                                                      17; Mismatches
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INFORMATION: ANT: Marc J.

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                                                                                 RESULT 13
US-08-530-950-13
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TITLE OF INVENTION:
D NUCLEIC ACIDS
NUMBER OF SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Patent No. 5470718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID
Sequence 13, Application US/08530950 Patent No. 5736381
GEMERAL INFORMATION:
APPLICANT: Davis, Roger J.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 26468
LENGTH: 787
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-16
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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TITLE OF INVENTION:
FILE REFERENCE: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/954,417
FILING DATE: 30.SEP-1992
PRIOR APPLICATION DATA;
APPLICATION NUMBER: 561,553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 561,553
FILING DATE: 01-AUG-1990
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27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  2 KGFTATLFLWTLIFPSCSGGGGGKAWPTHVVCSDSGLEVLYQSCDFLQDFGFSVEKCSKQ 61
                                                                                                                                                                    CPIAFELNFGNPDRCKTPEQYSRGEVFTRRFLGEFNFPQGEHMTWVKFW 307
                                                                                                                                                                                                             LP----KFSFCGRRKGEQIYYAGPVNN----PEFTIPQGEYQVLLELY 145
                                                                                                                                                                                                                                                      -RSDILWQASLITMAAETDDELGLVLAAPAHSASGLYRRVIEIDGRRIYTDFSVTIPSER 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDPLQDFGFSVEKCSKQLKSNINIRFGI-----ILREDIKELFLDLALMSQGSSVL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O'CALLAGHAN, DENNIS J.
NVENTION: EQUINE HERPESVIRUS TYPE 1 GLYCOPROTEIN
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25.4%; Pred. No. 3.1;
ative 16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                          63; Indels
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US-09-149-879-13

Sequence 1 Patent No.

13,

Application US/09149879 6174676

GENERAL INFORMATION:

APPLICANT: Davis, Roger J.
APPLICANT: Raingeaud, Joel
APPLICANT: Gupta, Shashi
APPLICANT: Derijard, Benoit
TITLE OF INVENTION: CYTOKINE-, STRESS-, AND
TITLE OF INVENTION: COCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street

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RESULT 14
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                           Query Match
Best Local (
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ZIP: 02110-2804
COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 19-5EP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORWATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,98
REFERENCE/DOCKET NUMBER: 0
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ADDRESSEE: I
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 668 amino acids
TYPE: amino acid
STRANDEDNESS: not releva
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                                                                                        139 - OVLLELYTEKRSTVA 153
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                                                                                                                                                                88 MSQGSSVINFSYPICEAALPKFSFCGRRKGEQIY--YAGPVNNPEFTIPQGEY-----
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                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                           h 8.2%; Score 71; DB 1; Length 668
Similarity 24.3%; Pred. No. 6.4;
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                                                        VSLCLQKIPERRPTYA 615
                                                                                                                           YTVQSDIWSLGLSILEMALGRYPY-PPETYDNIFSQLSAIVDGPPPRLPSDKFSSDAQDF 599
                                                                                                                                                                                                                                   PTHYVCSDSGLEVLYQSCDPLQDFGFSVEKCSKQLKSNINIRFGIILREDIKELFLDLAL
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E: Fish & Richardson P.C.
225 Franklin Street
                                                                                                                                                                                                                                                                        Conservative
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VENTION: CYTOKINE-, STRESS-, AND
VENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
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                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                          24; Mismatches
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                                                                                                                                                                                                                                                                          61; Indels
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US-09-057-009-13
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COUNTRY: USA
ZIP: 02110-2804
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/149,879
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Patent No. 6541605
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Best Local S
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Raingeaud, Joel
APPLICANT: Raingeaud, Joel
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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NAME: FASSE, J. Peter
REGISTRATION UNDER: 32,983
REFERENCE/DOCKET NUMBER: 0791
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                          NPPLICANT: Derijard, Benoit
TITLE OF INVENTION: CYTOXINE-, STRESS-, AND
TITLE OF INVENTION: ONCOPROTEIN-ACTIVATED HUMAN PROTEIN KINASE
TITLE OF INVENTION: KINASES
TUMBER OF SEQUENCES: 16
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TYPE: amino acid
STRANDEDNESS: not releva
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                                                                                                               COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                  CITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 MSQGSSVLNFSYPICEAALPKFSFCGRRKGEQIY--YAGPVNNPEFTIPQGEY----- 138
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                                                                                                                                                            Boston
: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09057009
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Search completed: April 29, 2004, 15:23:47 Job time : 23 secs
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                                                                                                                                                                                                                                                                                                                                                         Query Match 8.2%; Score 71; DB 4; Length 668; Best Local Similarity 24.3%; Pred. No. 6.4; Matches 33; Conservative 24; Mismatches 61; Indels
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTION NUMBER: 32,983
REFERENCE DOCKET NUMBER: 07917/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 668 amino acids
TYPE: amino acid
STRANDEDRESS: NO. 6541605 Relevant
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/057,009
                                                                                                                                                                                                                                                                   488 PTNILCSAN------OGTVKLCDFGVSGNLVASLAKTNIGCO-SYMAPERIKSLNPDRAT 540
                                                                                           600 VSLCLQKIPERRPTYA 615
                                                                                                                                 139 -QVLLELYTEKRSTVA 153
                                                                                                                                                                               541 YTVQSDIWSLGLSİLEMALGRYPY-PPETYDNİFSQLSAIVDGPPPRLPSDKFSSDAQDF 599
                                                                                                                                                                                                                                                                                                                28 PTHVVCSDSGLEVLYQSCDPLQDFGFSVEKCSKQLKSNINIRFGIILREDIKELFLDLAL
                                                                                                                                                                                                                          88 MSQGSSVLNFSYPICEAALPKFSFCGRRKGEQIY--YAGPVNNPEFTIPQGEY----- 138
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Result
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Maximum DB
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Maximum Match 100%
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613
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101.5
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81.5
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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Match
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l: /cgn2_6/ptodata/2/pubpaa
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Copyright (c) 1993 - 2004 Compugen Ltd.
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/ Ggn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/ Ggn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/ Ggn2_6/ptodata/2/pubpaa/US09_REMP PUB_PEP:*
/ Ggn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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   6/ptodata/2/pubpaa/PCTUS PUBCOMB.pep:*
6/ptodata/2/pubpaa/US08 NEW PUB.pep:*
6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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US-09-372-348-23

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2 US-10-000-066-13
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   US-10-424-599-214951
US-10-424-599-199134
US-10-282-122A-77326
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Sequence 2, Appli
Sequence 13, Appl
Sequence 19, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 29, Appli
Sequence 29, Appli
Sequence 23, Appli
Sequence 1, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 26, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
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Sequence 21, Appl
Sequence 21, Appl
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US-09-899-917-2
     INFORMATION FOR
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76.	•	3	1 12	S-10-282-122A-4591	equence 4591
7 75.5 75.5	00 00 00 00	1241	2 2	US-10-282-122A-54490 US-10-282-122A-51957	e 54490, e 51957,
7		0	<u>⊬</u> 1	9-10-205-823-427	equence 427, Ap
7	•	0	14	S-10-354 - 358-9	equence 98, App
7	•	N	12	-10-087-192-8	equence 84, App
7		ω	9	-09-925-300-153	quence 1538,
72.		~1	12	S-10-363-616-4	equence 446,
72.		17	12	-10-363-616-44	equence 445, Ap
7		26	12	-10-425-114-5380	equence 53807,
7		on.	12	-10-425-114-53	equence 538
7		ത	12	-10-425-114-6847	equence 68478,
71.		_	15	-10-041-615-2	equence 28, Ap
7	٠	ω	9	S-09-761-569-1	quence 13,
7		O.	9	09-801-368-23	equence 238, App
7		O.	14	-10-081-119-20	equence 20, App
7		an.	15	S-10-369-493-2	equence 221
7		\mathbf{r}	14	-10-260-715-6	equence 6, Appl
		(n	14	10-260-715-4	Sequence 4, Appl
70.		\mathbf{L}	10	-09-372-348-	equence 25, App
70.		\mathbf{L}	12	S-10-000-066-	equence 4, App
70.		\rightarrow	12	-10-335-977-627	equence 627
70.		10	12	-10-424-599-	equence 234625,
J		1.4	12	-10-282-122A-7750	equence 77503,
- 3		in	15	-10-264-237-164	equence 16
~1		•	11	-09-833-245-169	equence 1692,
~1		_	15	-10-369-493-1747	equence 17475,
~ 1		t m	<u>1</u> 5	-10-369-493-219	equence 21918
69.		in	12	0-424-599-2340	equence 23
69.	ם	. 1	<u>_</u>	-10-434-418-	equence 2, Ap

ALIGNMENTS

Sequence 2, Application US/09899917
Patent No. US20020119552A1
GENERAL INFORMATION: COUNTRY: USA
ZIF: 20005-3934
ZIF: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PILING DATE: 09-UH-2001
CLASSIFICATION: CUnknown> PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/994,962
FILING DATE: «Unknown»
APPLICATION NUMBER: US 60/037,388
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION: CORRESPONDENĈE ADDRESS:
ADDRESSEE: Sterne, Kessler Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington APPLICANT: Olsen, Henrik S.
Ruben, Steven M.
TITLE OF INVENTION: Human Oncogene Induced Secreted Protein I
NUMBER OF SEQUENCES: 17 TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
TELEPAX: DI NO: 2: NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0440002

SEQUENCE CHARACTERISTICS: LENGTH: 162 amino acids TYPE: amino acid

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;
TOPOLOGY: linear
;
MOLECULE TYPE: procein
;
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-899-917-2
RESULT 3
US-09-372-348-19
; Sequence 19, Application US/09372348A
; Publication No. US20030028005A1
; GENERAL INFORMATION:
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US-10-000-066-13
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Publication No. US20020086364A1

GENERAL INFORMATION:
APPLICANT: HONJO, TASUKU
APPLICANT: KATO, KEIZO
APPLICANT: TADA, HIDEAKI
TITLE OF INVENTION: POLYPEPTIDE, cDNA ENCODING THE SAME, AND USE OF THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/JP98/04515
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: HEI-9-274673
PRIOR FILING DATE: 1997-10-07
NUMBER OF SEC ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: Q58771
CUTRENT APPLICATION NUMBER: US/10/000,066
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/529,064
PRIOR FILING DATE: 2000-04-17
PRIOR FILING DATE: 2000-04-17
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                                                                                                                                                                                                                  QLKSNINIRFGIILREDIKELFLDLALMSQGSSVLNFSYPICEAALPKFSFCGRRKGEQI
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121 YYAGPVNNPEFTIPQGEYQVLLELYTEKRSTVACANATIMCS 162

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CURRENT APPLICATION NUMBER: US/09/372,348A; CURRENT FILING DATE: 1999-08-11; NUMBER OF SEQ ID NOS: 29; SOFTWARE: PATENTIN Ver: 2.0; SEQ ID NO 19; LENGTH: 162; TYPE: PRT; ORGANISM: primate
US-09-372-348-19
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hedrick, Joseph A.
APPLICANT: Wang, Luquan
APPLICANT: Wang, Luquan
APPLICANT: Murgolo, Nicholas J.
APPLICANT: Murgolo, Nicholas J.
APPLICANT: Greene, Jonathan R.
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: Mammalian Proteins; Related Reagents and Methods
FILE REFERENCE: DX0884K(2d)
CURRENT APPLICATION NUMBER: US/09/372,348A
CURRENT FILING DATE: 1999-08-11
NUMBER OF SEQ ID NOS: 29
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 27
TENTED: 150
                                                                                                                                                                                                                                                                 ; LENGTH: 162
; TYPE: PRT
; ORGANISM: rodent
US-09-372-348-27
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Best Local :
                                                                                                                                                                       Query Match 71.1%; Score 613; DB 10
Best Local Similarity 66.7%; Pred. No. 5e-64;
Matches 108; Conservative 22; Mismatches
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APPLICANT: Wang, Luquan
APPLICANT: Zlotnik, Albert
APPLICANT: Murgolo, Nicholas J.
APPLICANT: Greene, Jonathan R.
APPLICANT: Johnston, James A.
APPLICANT: Johnston, James A.
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: Mammalian Proteins, Related Reagents and Methods
FILE REFERENCE: DX0884K(2d)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 QLKSNINIREGIILREDIKELFLDLALMSQGSSVLNESYPICEAALPKFSFCGRRKGEQI 120
       61
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                                                                                  1 MNGVAAALLVWILTSPSSSDHGSENGWPKHTACNSGGLEVVYQSCDPLQDFGLSIDQCSK 60
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  QLKSNINIRFGIILREDIKELFLDLALMSQGSSVLNFSYPICEAALPKFSFCGRRKGEQI 120
                                                                                                                                    MKGFTATLFLWTLIFPSCSGGGGKAWPTHVVCSDSGLEVLYQSCDPLQDFGFSVEKCSK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09372348A
c. US20030028005A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 850; DB 10;
Pred. No. 4.8e-92;
                                                                                                                                                                                                                         DB 10; Length
                                                                                                                                                                              32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 162;
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                                                                                                                                                                              Gaps
           120
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121

YYAGPUNNPGLDVPQGEYQLLLELYNENRATVACANATVTSS 162

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US-10-000-066-10
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US-09-899-917-3
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TYPE: PRT
GRGANISM: Mus musculus
US-10-000-066-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: HONJO, TASUKU
APPLICANT: KATO, KEIZO
APPLICANT: TADA, HIDBAKI
TITLE OF INFORMATION: POLYPEPTIDE, CDNA ENCODING THE SAME, AND USE OF THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/10000066 Publication No. US20020086364A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09899917
Patent No. US20020119552A1
GENERAL INFORMATION:
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Best Local :
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CURRENT APPLICATION NUMBER: US/10/000,066
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/529,064
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: PCT/JP98/04515
PRIOR FILING DATE: 1998-10-06
PRIOR FILING DATE: 1998-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: HEI-9-274673 PRIOR FILING DATE: 1997-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                           ZIP: 20005-3934
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/899,917
FILING DATE: 09-UL-2001
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Olsen, Henrik S.
Ruben, Steven M.
                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Human Oncogene Induced Secreted Protein NUMBER OF SEQUENCES: 17
  PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 QLKSNINIRFGITLREDIKELFLDLALMSQGSSVLNFSYPICEAALPKFSFCGRRKGEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MXGFTATLFLWTLIFPSCSGGGGKAWPTHVVCSDSGLEVLYQSCDPLQDFGFSVEXCSK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MNGVAAALLVWILTSPSSSDHGSENGWPKHTACNSGGLEVVYQSCDPLQDFGLSIDQCSK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YYAGPVNNPGLDVPQGEYQLLLELYNENRATVACANATVTSS 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YYAGPVNNPEFTIPQGEYQVLLELYTEKRSTVACANATIMCS 162
APPLICATION DATA:
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                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 12; Length 162;
                                                                                                               Version #1.30
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APPLICANT: Hedrick, Joseph A.
APPLICANT: Wang, Luquan
APPLICANT: Wang, Luquan
APPLICANT: Murgolo, Nicholas J.
APPLICANT: Murgolo, Nicholas J.
APPLICANT: Greene, Jonathan R.
APPLICANT: Johnston, James A.
APPLICANT: Johnston, James A.
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: Mammalian Proteins; Related Reagents and Methods
FILE REFERENCE: DX0804K(2d)
CURRENT APPLICATION NUMBER: US/09/372,348A
CURRENT APPLICATION NUMBER: US/09/372,348A
CURRENT FILING DATE: 1999-08-11
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 29
LENGTH: 160
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Best Local S
Matches 60
                                                                                                                                      Best Loc
Matches
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                                                                                                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 133 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDENNESS: No. US20020119552A1 Relevant
TOPOLOGY: No. US20020119552A1 Relevant
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: <UNKNOWN>
APPLICATION NUMBER: US 60/037,388
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 WPTHVVCSDSGLEVLYQSCDPLQDFGFSVEKCSKQLKSNINIRFGIILREDIKELFLDLA 86
                                                                                                                                         59.
87 LWSQGSSYLWFSYPICEAALPKFSFCGRRKGEQIYYAGFVMVPEFTIFQGEYQVLLELYT 146
                                                                                        27 WPTHVVCSDSGLEVLYQSCDPLQDFGFSVEKCSKQLKSNINIRFGIILREDIKELFLDLA 86
                                                22 WPTHTVCKEENLEIYYKSCDPQQDFAFSIDRCSDVTTHTFDIRAAMVLRQSIKELYAKVD 81
                                                                                                                                    h 39.0%;
Similarity 44.4%;
59; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPTHTVCKEBNLEIYYKSCDPQQDFAFSIDRCSDVTTHTFDIRAAMVLRQSIKELYAKVD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDRATVACADETY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKRSTVACANATI 159
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Wo. US20030028005A1
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ilarity 45.1%;
Conservative 26
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; Pred. No. 2.4e-32;
26; Mismatches 47
                                                                                                                                    ; Score 336; DB 10;
; Pred. No. 2.8e-31;
26; Mismatches 48;
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                                                                                                                                                                               Length 160;
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                                                                                                                                         Indels
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LIINGKTVLSYSETLCGPGLSKLIFCGKKKGEHLYYEGPITLGIKEIPORDYTITARLTN 141

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EKRSTVACANATI 159

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PRIOR APPLICATION NUMBER: 09/229,064
PRIOR APPLICATION NUMBER: 09/229,064
PRIOR APPLICATION NUMBER: 09/229,064
PRIOR APPLICATION NUMBER: PCT/JP98/04515
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: HEI-9-274673
PRIOR FILING DATE: 1997-10-07
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
; SEQ ID NO 23
; LENGTH: 160
; TYPE: PRT
; ORGANISM: primate
US-09-372-348-23
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; ORGANISM: Mus musculus
US-10-000-066-1
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Publication No. US20020086364A1
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23, Application US/09372348A Publication No. US20030028005A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                    APPLICANT: Wang, Luquan
APPLICANT: Zlotnik, Albert
APPLICANT: Murgolo, Nicholas J.
APPLICANT: Greene, Jonathan R.
APPLICANT: Johnston, James A.
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: Mammalian Proteins; Related
FILE REFERENCE: DX0884X(2d)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: HONJO, TASUKU
APPLICANT: KATO, KEIZO
APPLICANT: KATO, KEIZO
APPLICANT: TADA, HIDEAKI
TITLE OF INVENTION: POLYPEPTIDE, CDNA ENCODING THE SAME, AND USE OF THEM
FILE REFERENCE: QS8771
CURRENT APPLICATION NUMBER: US/10/000,066
CURRENT FILING DATE: 2001-12-04
CURRENT FILING DATE: 2001-12-04
                                                                                                                                         CURRENT FILING DATE: 1999-08-11
NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hedrick, Joseph A.
                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/372,348A
CURRENT FILING DATE: 1999-08-11
                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
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les 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -SVNSIELPKRKEVLCHGHDDDYSFCRALKGETVNTSIPFSFEGILFPKGHYRCVAEAIA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSYLNESYP----ICEAALPKESECGRRKGEQIYYAGPVNNPEFTIEQGEYQVLLELY- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNSSDAIISYSYCDHLKFPISISSEPCIRLRGTNGFVHVEF1PRGNLKYLYFNLFI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.3%; Score 106; DB 12; Length 160; 26.3%; Pred. No. 0.00044; tive 24; Mismatches 61; Indels 1
                                                                                                                                                                                                                                              Reagents
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US-09-372-348-26

Sequence 26, Application US/09372348A Publication No. US20030028005A1

GENERAL INFORMATION:
APPLICANT: Hedrick, Joseph A.
APPLICANT: Wang, Luquan
APPLICANT: Zlornik, Albert
APPLICANT: Murgolo, Nicholas J.
APPLICANT: Greene, Jonathan R.
APPLICANT: Greene, Jonathan R.

INVENTION: Mammalian

Proteins; Related Reagents and Methods

Johnston, James A. Bazan, J. Fernando

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                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-000-066-7
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US-10-000-066-7
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                                                                                                                                                                                                                                                                       Best Local
                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: Q58771
CUTRENT APPLICATION NUMBER: US/10/000,066
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/529,064
PRIOR FILING DATE: 2000-04-17
PRIOR FILING DATE: 2000-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/JP98/04515
PRIOR FILING DATE: 1998-10-06
PRIOR APPLICATION NUMBER: HEI-9-274673
PRIOR FILING DATE: 1997-10-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HONJO, TASUKU
APPLICANT: KATO, KEIZO
APPLICANT: TADA, HIDBAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLE OF INVENTION: POLYPEPTIDE, CDNA ENCODING THE SAME, AND USE OF THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 AGPVNNPEFTIPQGEYQVLLE 143
                                     123 AGPVNNPEFTIPQGEYQVLLE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 GSKGLLHIFYIPRRDLKQLYFNLYITVNTMNLPKRKEVICRGSDDDYSFCRALKGETVNT 115
                                                                              56 GSKGLLHIFYIPRRDLKQLYFNLYITVNTMNLPKRKEVICRGSDDDYSFCRALKGETVNT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 FTATLFLWTLIFPSCSGGGGGKAWPTHVVCSDSGLEVLYQSCDPLQ-DFGFSVEKCSKQL 62
                                                                                                                                                                                                      4 FTATLFLWTLIFPSCSGGGGKAWPTHVVCSDSGLEVLYQSCDPLQ-DFGFSVEKCSKQL
                                                                                                                                                                                                                                                 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FFSTLF--SSIFT-----EAQKQYWVCNSSDASISYTYCDKWQYFISINVNPCIELK 55
                                                                                                                                                            FESTLE--SSIFT-----EAQKQYWVCNSDASISYTYCDKWQYPISINVNPCIELK 55
                                                                                                                    KSNINIRFGIILREDIKELFLDLALMSQGSSVLNFSYPICEAALPKFSFCGRRKGEQIYY 122
TISFSFKGIKFSKGKYKCVVE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                              11.8%; Score 101.5; DB 12; 24.1%; Pred. No. 0.0015; tive 26; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                         DB 12;
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                                                                                                                                                                                                                                                                                           Length 160;
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FILE REFERENCE: DX0884K(2d)

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RESULT 12
US-09-899-917-17
Sequence 17, Application US/09899917
Patent No. US20020119552A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/372,348A
CURRENT FILING DATE: 1999-08-11
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 26
LENGTH: 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.2%; Score 96.5; DB 10; Length 141; Best Local Similarity 25.6%; Pred. No. 0.0049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/994,962
FILING DATE: «Unknown»
APPLICATION NUMBER: US 60/037,388
FILING DATE: 07-FEB-1997
ATTORNEY,AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REGISTRATION NUMBER: 1488.0440002
TELEPHONE: 202-371-2540
TELEPHONE: 202-371-2540
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIF: 20005-3934

ZIF: 20005-3934

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW, Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Olsen, Henrik S.
Ruben, Steven M.
                                                                                    STRANDEDNESS: single
TOPOLOGY: No. US20020119552A1 Relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Human Oncogene Induced Secreted Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 -SVNSIELPKRKEVLCHGHDDDYSFCRALKGETVNTSIPFSFEGILFPKGHYRCVAE 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/899,917 FILING DATE: 09-Jul-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                LENGTH: 60 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
10.9%;
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Score 94; DB 9;
Pred. No. 0.003;
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                      Length 60;
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US-10-424-599-214951
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US-10-424-599-199134
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US-10-424-599-214951
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SEQ ID NO 214951
LENGTH: 555
TYPE: PRI
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                                                                                                                                                                                                                                                             Sequence 199134, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 199134
LENGTH: 170
TYPE: PRT
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
                                                                       APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)|B
FULL REFERENCE: 38-21(5323)|B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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NAME/KEY: unsure
LOCATION: (1)...(555)
OTHER INFORMATION: unsure at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 LODFGFSVEKCSKOLKSNINIRFGIILREDIKELFLDLALMSOGSSVLNFSYPICEAALP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cn 9.5%; Score 81.5;
1 Similarity 25.7%; Pred. No. 1.
26; Conservative 18; Mismatche
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59
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; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-282-122A-77326
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US-10-424-599-199134
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/20, 848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-26
PRIOR PILING DATE: 2000-12-26
PRIOR PILING DATE: 2001-12-7
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PILING DATE: 2000-12-26
PRIOR PILING DATE: 2001-12-7
PRIOR PILING DATE: 2001-12-7
PRIOR PILING DATE: 2001-12-7
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PRIOR PILING DATE: 2001-12-7
PRIOR PILING DATE: 2001-12-7
PRIOR PILING DATE: 2001-12-7
PRIOR PILING DATE: 2001-12-7
                                                                                                                       Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 77326
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Publication No. US20040029129A1
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLICANT:
                                                                                             ENGTH: 876
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Local Similarity 21.1%; Pred. No. 0.43;
nes 35; Conservative 20; Mismatches 59; Indels 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 LKKGE-LSLTKDVELPR-EIPPGTYTVLADVYTEDGDKITCLTAKI 166
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INVENTION: Identification of Essential Genes in Microorganisms
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Wall, Daniel
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Yamamoto, Robert
Forsyth, R.
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Malone, Cheryl
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Query Match

9.0%;

Score 78;

DB 12;

Length 876;

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688 VCG--NNPNCEGFIVEEGEFKV
                                      122 YAGPVNNPE---FTIPQGEYQV 140
                                                                              641 INLGDEEGVINVLEEDVE----TAALRAKKRC-----PICETAMDAYLIDDKRK---LH 687
                                                                                                                                                                                                 8 LFLWTLIFPSCSGGGGGKAWPTHVV--CSDSGLEVLYQSCDPLQDFGFSVEKCSKQLKSN 65
                                                                                                              INI--REGII--LREDIKELELDLALMSQGSSVLNESYPICEAALPKESECGRRKGEQIY 121
707
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Search completed: April 29, 2004, 15:29:31 Job time: 43 secs

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Maximum Match 100%
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742.049 Million cell updates/sec
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2: pir2:*
3: pir3:*
4: pir4:*
  MKGFTATLFLWTLIFPSCSG......ELYTEKRSTVACANATIMCS 162
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       parameters:
                                                                                                                                                                                                                                                                                               copia-like retroel
hypothetical prote
probable triacylyl
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           DNA recombinase (r
glutamate receptor
ABC transporter, A
DNA-directed RNA p
polymyxin B resist
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S-locus-specific g
probable exported
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                                                                          conserved hypothet
RESULT 2

GR45B1

copia-like retroelement pol polyprotein [imported] - Arabidopsis thaliana

copia-like retroelement pol polyprotein [imported] - Arabidopsis thaliana

copia-like retroelement pol polyprotein [imported] - Arabidopsis thaliana

copia-like retroelement pol polyprotein [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Decies: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: G845B1

C;Accession: G845B1

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.

R;Lin, X.; Kaul, S.; Cronin, L.A.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.

R;Lin, X.; Kaul, S.; Cronin, L.A.; Shea, M.; VanAken, S.E.; Umayam, L.; Tallon,

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
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S18633
MD-1 protein - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Sep-1999
C;Accession: S18633; 842854
R;Burk, O.; Klemphauer, K.H.
BMBO J. 10, 3713-3719, 1991
A;Title: Estrogen-dependent alterations in differentiation state of myeloid A;Reference number: S18633; MUID:92037533; PMID:1718743
A;Accession: S18633
A,Molecule type: mRNA
A;Residues: 1-160 <BURN
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A;Residues: 1-160 <BURN
A;R A;Molecule type: mRNA A;Residues: 1-130,'R',132-160 <BUZ> A;Cross-references: EMBL.X60450; NID:g432637; PID:g432638 C;Superfamily: chicken MD-1 protein R;Burk, O.
submitted to the EMBL Data
A;Reference number: S42854
A;Accession: S42854 A;Cross-references: EMBL:X60450 R;Burk, O. A;Status: preliminary 22 WPTHTVCKEENLEIYYKSCDPQQDFAFSIDRCSDVTTHTFDIRAAMVLRQSIKELVAKVD 81 60; h 39.9%; Score 344; DB 2; Length 160; Similarity 45.1%; Pred. No. 2.6e-27; 60; Conservative 26; Mismatches 47; Indels WPTHYVCSDSGLEVLYQSCDPLQDFGFSVEKCSKQLKSNINIRFGIILREDIKELFLDLA 86 EDRATVACADETV LIINGKTVLSYSETLCGPGLSKLIFCGKKKGEHLYYEGPITLGIKEIPQGDYTITARLTN 141 imsogssylvesypiceaalpxesecgrrkgeqiyyagpynnesetipogeyQvileiyt 146 EKRSTVACANATI 159 Library, September 1991 154 <u>,</u> of myeloid cells caused Gaps 0,

C.Y.; N llon, L.: enter, J.

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A;Reference number: A8442
A;Accession: G84581
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1137 <STO>
A;Cross-references: GB:AE
C;Genetics:
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probable triacylglycerol lipase [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: H84723 C;Accession: H84723 Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.;
                                                                                            RESULT
H84723
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DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: H71139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein PH0331 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 28-Jul-2000
C;Accession: H71139
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A;Experimental source: strain OT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-406 <K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Note: this accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; nucleic acid sequence not shown; translation
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Best Local
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Map position: 2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -406 <KAW>
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                                                                                                                                                                                                                                                                                                                MKGASFFVTLFLWFIVMSLIFGVPGKLAVFPLLLLI----MGLLF---DAPGDFEVEREI
                                                                                                                                                              --FTYPGRRSFQLSYKLLPLKRGVYEIPKTE 132
                                                                                                                                                                                                    PKFSFCGRRKGEQIYYAGPVNNPEFTIPQGE 137
                                                                                                                                                                                                                                         EKAQTFVGNEIEVLVRVRVGRGIGLVMVRENIPKAF----MTSSGSNVGYF--
                                                                                                                                                                                                                                                                           EKC----SKQLKSNINIRFG-----IILREDIKELFLDLALMSQGSSVLNFSYPICEAAL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved
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25.8%;
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                                                                                                                                                                                                                                                                                                                                                                                      Score 81; DB 2; Length 406; Pred. No. 2.6; Indels 27; Mismatches 49; Indels
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Pred. No. 0.13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 accession
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       Town, C.D.; Fujii,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: BB2163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA topoisomerase I VC1730 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: B82163
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A; Residues: 1-484 <STO>
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A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: GB:AE004251; GB:AE003852; NID:g9656248; FIDN:AAF94880.1; GSPDB:GN001;
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
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A;Map position: 1
C;Superfamily: bacterial type I DNA topoisomerase
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                                                                             641
                                                                                                                                                       599 IVMTNILCPTCSRPMGIRTASTGVFLGCSGYGLP--
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                                     122 YAGPVNNPE---FTIPQGEYQV 140
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                                                                                                          66 INI--REGII--LREDIKELFLDLALMSQGSSYLNFSYPICEAALPKFSFCGRRKGEQIY 121
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  VCG-
                                                                             INLGDEEGVINVLEEDVE - - - - TAALRAKKRC - -
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ilarity 27.4%;
Conservative 1
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                                                                                                                                                                                                                                    9.0%; Score 78; DB
26.1%; Pred. No. 13;
ative 23; Mismatches
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Pred. No. 4.6;
18; Mismatches
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A;Cross-references: SGD:S0006226
A;Map position: 16R
C;Keywords: transmembrane protei
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A75012
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A; Accession: A75012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conserved hypothetical protein PAB1277 - Pyrococcus abyssi (strain Orsay) C;Species: Pyrococcus abyssi (C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 28-Jul-20 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #sequence_revision 20-Aug-1999 #s
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A; Residues: 1-1133 <BAD>
A; Cross-references: EMBL: Z49274; NID:g809585;
A; Experimental source: strain AB972
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;Badcock, K.; Churc
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;768-784/Domain: transmembrane #status predicted
;931-947/Domain: transmembrane #status predicted
;971-987/Domain: transmembrane #status predicted
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Date: 08-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 19-Apr-2002;
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37; Conserv
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AALPKFSFCGRRKGEQIYYAGPVNNPEFTIPQGE 137
                                                                  EVTKRRVFVGEEVRVKLRVRVSKGIGIVILKENLPRAF-----EVKGSATFHFFTYPGKR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                     -CSKQLKSNINIRFG-----IILREDIKELFLDLALMSQGSSVLN-FSYPICE 103
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                                                                                                                                                                                                                                                                                                                                                              9.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein PAB1277
                                                                                                                                                                                                                                                                                                                                     31;
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                                                                                                                                                                                                                                                                                                                                                          Score 77.5; Ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 78; DE
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                     Pred. No. 5.7;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 1133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:g809587; GSPDB:GN00016; MIPS:YPR022c
                                                                                                                                                                                                                                                                                                                                                                                                        명
                                                                                                                                                                                                                                                                                                                                     44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <TM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <TMI>
                                                                                                                                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                    Length 394;
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPLRWIIFSHA 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62;
                                                                                                                                                                                                                                                                                                                                     43;
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                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                           51
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o-locus-specific glycoprotein - wild cabbage (fragment)
N;Alternate names: S glycoprotein
C;Species: Brassica oleracea (wild cabbage)
C;Date: 20-Sep_1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
C;Accession: T14529
R;Kusaba, M.; Nishio, T.; Safta v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable exported protein YPO3241 [imported] - Yersinia pestis (strain C;Species: Yersinia pestis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:D85205; NID:g2351141; PIDN:BAA21939.1; PID:g2351142
C;Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-428 < K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Striking sequence similarity in inter- and intra-specific comparisons of class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
                                                                                                                                                                                                                                       A; Gene: YPO3241
C; Superfamily:
                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Reeidues: 1-246 KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92476.1; PID:g15981177; GSPDB:GN00175
                                                                                                                                                                                                                                                                                                                                                                                                       Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Date: 02-Nov-2
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Best Local (
                                                                                                                                                             Matches
                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 OSFDFFTDTLLPEMKLGYNLKTGL-----NRFLTAWRNSDDPSSGDYSYKLENRELPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 FSFCGRRKGEQIYYAGPVNNPEFT-IPQGE-YQVLLELYTEKRSTVA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 QDFGFSVEKCSKQLKSNINIRFGIILREDIKELFLDLALMSQGSSVLNFSYPICEAALPK 108
                                      99
                                                                                                                  45 CDPLQDFGFSVEK---CSKQLKSNI---NIRFGIILREDIKELFLDLALMSQGSSVLNFS
  69
                                                                           13 CLPAASFTSSASEPVAVSKELKQQLLG8SVYIQIFKEERVLELYAKL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27;
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                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FYLL--KSGFQVHRSGPWNGVRFSGIPENQKLSYMVYNFTENSEEVA 246
                                    YPICEAALPKFSFCG-----RRKGEQIYYAGPVNNPEFTIPQGEYQV 140
                                                                                                                                                                                                                                           Escherichia coli probable membrane protein yafK
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                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z18078; MUID:97352858; PMID:9207151
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25.2%;
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29.0%;
  FSGGLGPKREG-
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Pred. No. 6.3;
                                                                                                                                                                               Score 77; DB:
pred. No. 3.8;
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                                                                                                                                                                30; Indels
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      -DFKSPEGFYRI
                                                                                                                                                                                                         Length 246;
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      96
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                                                                                    83
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S.; Barrell, E
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RESULT G96740

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R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; D. ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; I Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Royer, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F40G12.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Sep-2000 C;Accession: T22058 R;McMurray, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-739 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F14O23.20 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-294 <WIL>
A;Cross-references: EMBL:Z77661; PIDN:CAB01187.1; GSPDB:GN00023; CESP:F40G12.4
A;Experimental source: clone F40G12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: G96740
                                                                                                                                                                                                                                                                         A;Map position: 5
A;Introns: 59/3; 159/3; 262/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F40Gl2
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A,Reference number: Z19507
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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 VOGKGYK-DKCYEQIRKAVEDRFNRLLTLVFEDLK----
167
                                              87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 LQDFGFSVEKCSKQLKSNINIRFGIILR---EDIKELFLDLALMSQGSSVLNFSYPICEA 104
                                                                                                                                                                                     23;
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                                              LMSQGSSVLNFSYPICEAALPKFSFC 112
                                                                                             PAHGGCSDTYYRLNAQRCDAQKTMMEWEIEKQLERLPKFKNSTQVIAMCREIKECMEDLC
                                                                                                                                  PTHVVCSDSGLEVLYQSCDPLQD-FGFSVEKCSKQLKSNINIRFGIILREDIKELFLDLA 86
FTEDSQYEIEFSLAVPELTVSHFTVC
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                                                                                                                                                                                     Conservative
                                                                                                                                                                                                         8.9%;
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                                                                                                                                                                                     13;
                                                                                                                                                                                                            Score 76.5;
Pred. No. 5
                                                                                                                                                                                     Mismatches
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13;
                                                                                                                                                                                                                               DB 2;
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                                                                                             166
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war, K.;
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RESULT T28066

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hypothetical protein ZK867.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-452 <TEL>
A; Cross-references: GB: M86664; NID: g330791; PIDN: AAB02507.1;
A; Experimental source: strain Ab4p
R; Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.
Virology 189, 304-316, 1992
A; Title: The DNA sequence of equine herpesvirus-1.
A; Reference number: A41831; MUID: 92295566; PMID: 1318606
A; Contents: annotation; possible protein-coding frames
A; Contents: annotation; possible protein-coding frames
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycoprotein D precursor - equine herpesvirus 1
C;Species: equine herpesvirus 1
A;Note: host Equus caballus (domestic horse)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 16-Jul-1999
C;Accession: I36802; B36646; PQ0146
C;Accession: I36802; B36646; PQ0146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-436 < NHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: T28066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid ZK867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Nhan,
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                                                                                                                                                                                                                                                                                                                                                       A;Note: neither amino acid nor nucleotide sequence is given R;Audonnet, J.C.; Winslow, J.; Allen, G.; Paoletti, E. J. Gen. Virol. 71, 2969-2978, 1990
A;Title: Equine herpesvirus type 1 unique short fragment encodes glycoproteins with homol A;Reference number: A36646; MUID:91108393; PMID:2177089
A;Accession: B36646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               문
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                                                                                   A;Molecule type: DNA
A;Residues: 1-452 < ADV-
A;Residues: 1-452 < ADV-
A;Residues: 1-452 < ADV-
A;Residues: 1-452 < ADV-
A;Cross-references: GB:M86664; NID:g330791; PIDN:AAB02507.1; PID:g330863
A;Experimental source: strain Kentucky D
R;Elton, D.M.; Halliburton, I.W.; Killington, R.A.; Meredith, D.M.; Bonass, Gene 101, 203-208, 1991
Gene 101, 203-208, 1991
A;Title: Sequence analysis of the 4.7-kb BamHI-EcoRI fragment of the equine A;Reference number: JQ0998; MUID:91276272; PMID:1647359
A;Accession: PQ0146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J. submitted to GenBank, March 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U41039; PIDN:AAA82394.1; CESP:ZK867.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Description: The DNA sequence A;Reference number: A36805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
A;Molecule type: DNA
A;Residues: 292-452 <ELT>
A;Cross-references: GB:M36299; NID:g330787; PIDN:AAA66546.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 LFLDLALMSQGSSYLNFSYP--ICEAALPKFSFCGRRK-----GEQIYYAG---- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I36802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSVPLT---YSIPFRSIKQALELVEHQKMYIAAFENQTLLCT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---PVNNPEFTIPQGEYQVLLELYTEKRSTVAC-ANATIMCS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CKHPGABVEILKMIFRLIGVNYTMIDVWKKPGQQYDFGSKQKNGNWSGMIGLLQSDQLDM 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSDSGLE------VLYQSCDPLQDFGFSVEKCSKQLKSNINIRFGIILREDIKE 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGLSMRIAPEREEVVLFSYPTRVFETSIQSFPVSSRMLLLIILIATFFISQLYQTDMLAF 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Z20464
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21.0%; Pred. No. 8.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of equine herpesvirus-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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      PID:g808672
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                                                                                                                                                      the equine herpesvirus
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7:
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C;Genetics:
A;Gene: 72
C;Superfamily: herpesvirus glycoprotein D
C;Keywords: glycoprotein; transmembrane protein
C;Keywords: glycoprotein; tstatus predicted <SIG>
F;1-19/Domain: signal sequence #status predicted <MAT>
F;20-452/Product: glycoprotein D #status predicted <MAT>
F;399-419/Domain: hydrophobic <HYD>
F;399-419/Domain: transmembrane #status predicted <TW2>
F;404-422/Domain: transmembrane #status predicted <TW2>
F;103,111,347,396/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;347,396/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein (imported) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B86192
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, S.; Kim, C. C.A; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Anuthors: Hunter, J.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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E86192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-471 <STO>
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RESULT 15
D81306
probable UDP-N-acetylglucosamine-N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecapre
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Best Local
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Genetics:
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                                                                                                                                 352
                                                                                                                                                                                                                                  292 AQLLAYDIABLGMNQRRDEKPVPVTVFSFAGPRVGNLGFKKRCEELGVKVLRITNVNDPI 351
                                                                                                                                                                                                                                                                                                                                        237 ESGFLGLYTSGESESKFG--LESCREQLISEIS---RLMNKHKGEEISITLAGHSMGSSL 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 LKSNINIRFGII--LREDIKELFLDLALMSQGSSVL------NFSYPICEAA 105
                                                                                                                                                                                                                                                                                                                                                                                     35 DSGLEVIYOSCOPLODEGESVEKCSKOLKSNINIREGIILREDIKELELDIALMSOGSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
                                                                                                                                                                                                                                                                                         95 LN-FSYPICEAALPK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                         h 8.9%; Score 76.5; Di
Similarity 26.6%; Pred. No. 8.9;
33; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LP----KFSFCGRRKGEQIYYAGPVNN----PEFTIPQGEYQVLLELY 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -RSDILWQASLITMAAETDDELGLVLAAPAHSASGLYRRVIEIDGRRIYTDFSVTIPSER 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KTYSÄRL-TWFKIMPTC-----ATPIH-----DVSYMKCNPKLSFAMCDE----- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGFTATLFLWTLIFPSCSGGGGKAWPTHVVCSDSGLEVLYQSCDPLQDFGFSVEKCSKQ 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CPIAFEQNEGNEDRCKTPEQYSRGEVETRRFLGEENFPQGEHMTWLKFW 307
                                                                                                                                 TKLP
                                                                                                                                                                                   FTIP 134
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Pred. No. 8.5;
16; Mismatches
                                                                                                                                                                                                                                                                                       -FSFCGRRKGE-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                            -QIYYAGPVNNPE 130
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A,Gene: murG; Cj1039
C,Superfamily: murG protein
C,Keywords: glycosyltransferase; hexosyltransferase
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A; Residues: 1-342 < PAR>
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                                                                                                                                                                                                                                               A; Experimental source: serotype
                                                                                                                                              Query Match
Best Local S
Matches 37
                                                                                                                                                                                                                                    Genetics:
                                                                                               196 EQNIKIIHQ-CGK-NDF----EKCKKHYQS-LNIQADIFDFSLNLEEKWKN--ADLAISR 246
                                                 247
 298 LDÉF---
                      128 NPETTIPQGEYQVLLELYTEKRST 151
                                                                     35 DSGLEVLYQSCDPLQDFGFSVEKCSKQLKSNINIR-----FGIILREDIKELFLDLALMS 89
                                                                                                                                              1 Similarity
37; Conserv
                                                AGASTL---FELCANTLPTIFIPYPYAAKNHQYFNAKFLQDQALC---
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Search completed: April 29, 2004, 15:24:22 Job time : 23 secs

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MEDLINE-99180501; PubMed=10079183;

MEDLINE-99180501; PubMed=10079183;

Megum N.A., Tsuji S., Nomura M., Shida K., Azuma I., Hayashi A.,

Matsumoto M., Seya T., Toyoshima K.;

"Human MD-1 homologue is a BCG-regulated gene product in monocyt."

Its identification by differential display.";

Biochem. Biophys. Res. Commun. 256:325-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Williams S.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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92:2815-2822(1998).
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ra Y., Shimazu R., Miyake K., Akashi S., Ogata H.,	, Yamashita Y.,
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Best Local S
Matches 162
                                                                                                                        LY86_MOUSE
088188;
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CARBOHYD
VARIANT
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GO; GO:0006281; P:apoptosis; TAS.
GO; GO:0008283; P:cell proliferation; TAS.
GO; GO:0008283; P:cell proliferation; TAS.
GO; GO:0006959; P:humoral immune response;
InterPro; IPR003172; EI DerP2_DerF2.
InterPro; IPR003172; EI DerP2;
Pfam; PF02221; EI DerP2_DerF2; 1.
SMART; SM00737; MĪ; 1.
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EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: May cooperate with CD180 and TLR4 to mediate the innate immune response to bacterial lipopolysaccharide (LPS) and cytokine production. Important for efficient CD180 cell surface expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell surface.
-i- TISSUE SPECIFICITY: Highly
                                                                                                                                                                       MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
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                 Lymphocyte a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Sir
hes 162;
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SUBCELLULAR LOCATION: Extracellular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDUCTION: In
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AB020499; BAA76410.1; ALT_INIT.
AL031123; CAB76262.1; -.
BC038846; AAH38846.1; -.
; HGNC:16837; LY86.
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N-LINKED (GLCNAC. . .) (PO'
M -> V (in dbSNP:1802323).
/FTId=VAR_014539.
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LYMPHOCYTE ANTIGEN 86.
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Pred. No. 2e-82;
Mismatches
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L outstation -
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InterPro; IPR003172; EI_DerP2_DerF2.
Pfam; PF02221; EI_DerP2_DerF2; 1.
SMART; SM00737; ML; 1.
                                                                                                                                                                                                                                                                                                                                                                                     Immune response; Inflammatory response; Signal.
SIGNAL 1 19
CHAIN 20 162 LYMPHOCYTE ANTIGEN
CARBOHYD 96 96 N-LINKED (GLCNAC.
CARBOHYD 156 156 N-LINKED (GLCNAC.
EEQUENCE 162 AA; 17811 MW; EEDZSDEA64A937ZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Immunol. 165:1925-1932(2000).
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Gorczynski R.M.,
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Miyake K., Shimazu R., Kondo J., Niki T., A
Yamashita Y., Miura Y., Kimoto M.;
"Mouse MD-1, a molecule that is physically
positively regulates its expression.";
J. Immunol. 161:1348-1353(1998).
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB007599; BAA32399.1; -. MGD; MGI:1321404; Ly86.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell surface.
TISSUE SPECIFICITY: Highly expressed in
thymus, and at lower levels in kidney.
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                             YYAGPVNNPEFTIPQGEYQVLLELYTEKRSTVACANATIMCS
                                                                                                                         MKGFTATLFLWTLIFPSCSGGGGKAWPTHVVCSDSGLEVLYQSCDPLQDFGFSVEKCSK
                                                                                               QIQSNLNIRFGIILRQDIRKLFLDITLMAKGSSILNYSYPLCEEDQPKFSFCGRRKGEQI
                                                                                                                                                                                           MNGVAAALLVWILTSPSSSDHGSENGWPKHTACNSGGLEVVYQSCDPLQDPGLSIDQCSK
YYAGPVNNPGLDVPQGEYQLLLELYNENRATVACANATVTSS
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Rodentia;
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                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                     Score 613;
Pred. No. 1
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N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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Sciurognathi;
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thi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                  DB 1;
.5e-56;
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Burk O., Klemphauer K.-H.;
"Estrogen-dependent alterations in differentiation state of myeloid cells caused by a v-myb/estrogen receptor fusion protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Bone marrow;
MEDLINE=92037533; PubMed=1718743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYMPHOCYTE &
                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last seq
10-OCT-2003 (Rel. 42, Last annotation to the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
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Lymphocyte antigen 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
Bos taurus
Eukaryota;
                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Binds CD180 (By similarity).
SUBCELLULAR LOCATION: Extracellular; associated with CD180 at total surface (By similarity).
TISSUE SPECIFICITY: Detected in the macrophage-like 10.4 cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ls caused by a v-myb/estrogen receptor fusion protein.";
J. 10:3713-3719(1991).
FUNCTION: May cooperate with CD180 and TLR4 to mediate the innate immune response to bacterial lipopolysaccharide (LPS) and cytokine production. Important for efficient CD180 cell surface expression (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDUCTION: By myb.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pro; IPR00317; E1_DerP2_DerF2.
Pro; IPR007110; Ig-like.
PP00221; E1_DerF2_DerF2; 1.
; SM00737; ML; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82
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1 20 POTENTIAL.

21 160 LYMPHOCYTE ANTIGEN 86.

21 160 AA; 18114 MW; 6E3345141E33C007 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A
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                             (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                               STANDARD;
   Chordata;
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Last annotation updat
precursor (MD-2 prote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 336;
Pred. No.
Craniata; Vertebrata; Euteleostomi,
                                                                                                                                                                                                                                                                               PRT;
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                                                                                                  n update)
Protein)
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P58755;
P58755;
Rel. 41, Cr
28-FEB-2003 (Rel. 41, Lr
10-CCT-2003 (Rel. 42, L
       Lymphocyte antigen 96
LY96 OR MD2.
Cricetulus griseus ((
Eukaryota, Metazoa, (
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CRIGR

STANDARD;

PRT;

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Created)

precursor Last sequence up

(MD-2

protein)

update)

(Chinese hamster). ; Chordata; Craniata; Vertebrata; Euteleostomi;

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Matches
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Guionaud C.T., Dubey (
"Role of bovine TLR2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immune response; Inflammatory response; Signal; Glycop SIGNAL 1 16 POTENTIAL.
CHARL 17 160 LYMPHOCYTE ANTIGEN 96.
DISULFID 95 105 BY SIMILARITY.
CARBOHYD 26 26 N-LINKED (GLCNAC. ...) (P CARBOHYD 114 114 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINKED (GLCNAC. ...) (P CARBOHYD 150 N-LINK
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InterPro; IPR007110; Ig-like.
Pfam; PF002221; E1_DerP2_DerF2; 1.
smarr; sm00737; ML; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 constituents
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF368418; AAL16721.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Loca1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Heterogeneous homopolymer formed from homodimers; disulfide-linked. Belongs to the lipopolysacharide (LPS) receptor, a multi-protein complex containing at least CD14, and TLR4. Binds to the extracellular domains of TLR2 and TL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Extracellular (By similarity).
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                                                                                                                                                                                                                              NIRFGIILREDIKELFIDLALMSQGSSVLNFSYP-----ICEAALPKFSFCGRRKGEQIY 121
                                                                           YAGPVNNPEFTIPQGEYQVLLELYT-EKRSTVACANATIM 160
                                                                                                                                                           HLYY--IARRDIQKLYLNLHI-----SIKSMTLPMRKEVICREYGGDYSFCGALKGETVN
                                                                                                                                                                                                                                                                                                                                                                                          LWILIFPSCSGGGGGKAWPTHVVCSDSGLEVLYQSCDFLQ-DFGFSVEKC--SKQLKSNI
TTIPFSFQGIRFSPGQYHCVVEAISGNSEEMLFCLNFTII
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, TLR4 and CD14 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29;
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the recognition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 160;
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            154
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Best Local S
Matches 33
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J. Exp. Med. 194:79-88 (2001).

-:- FUNCTION: Cooperates with TLR4 in the innate immune response to bacterial lipopolysaccharide (LPS), and with TLR2 in the response to cell wall components from Gram-positive and Gram-negative bacteria. Enhances TLR4-dependent activation of NF-kappa-B. Cells expressing both ND2 and TLR4, but not TLR4 alone, respond to LPS (By similarity).

-!- SUBUNIT: Heterogeneous homopolymer formed from homodimers; disulfide-linked. Belongs to the lipopolysaccharide (LPS) receptor, a multi-protein complex containing at least CD14, LY96 and TLR4. Binds to the extracellular domains of TLR2 and TLR4 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immune response;
Polymorphism.
SIGNAL 1
CHAIN 17
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CARBOHYD
VARIANT
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CARBOHYD
CARBOHYD
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or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF325501; AAK57984.1; -.
InterPro; IPR003172; E1_DerP2_DerF2.
InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cricetulus.
NCBI_TaxID=10029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02221; E1 D
SMART; SM00737; ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21329172; PubMed=11435474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Ovarian carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
SUBCELLULAR LOCATION: Extracellular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration even the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way fitled and this statement is not removed. Usage by and for commercial tites requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
145
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                                                                                                                                                                                                                                                                    Similarity
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KLFCLNFTII
                                                                                I EVPTRKEI I CHGYDDNYSFCKALKGETVNTVVPFSFKGILFPKGQYRCVAEAI VGDNEE
                                                                                                                        SSVINFSYPICEAALPKFSFCGRRKGEQIYYAGPVNNPEFTIPQGEYQVLLE-LYTEKRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inflammatory response; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _DerP2_DerF2; 1
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105
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154
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                                                                                                                                                                                                                                                14.4%; Score 124; D
25.4%; Pred. No. 1e-
tive 23; Mismatches
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                                                                                                                                                                                                                                                                                                                                                  LYMPHOCYTE ANTIGEN 96.
BY SIMILARITY.
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                        <u>ب</u>
                                                                                                                                                                                                                                                  72;
                                                                                                                                                                                                                                                                                        Length 160;
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LY96 MOUSE
ID LY96 MOUSE
AC Q9JHF9;
DT 28-FEB-2003

STANDARD;

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RA Kawai J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., RA Kawai J., Shinagawa A., Fukunishi Y., Konno H., Adachi J., Fukuda S., RA Airawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Ajato T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Ra Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ra Kuchi P., Lawis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Ra Kuchi P., Lawis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Ra Kuchi P., Lawis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Ra Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Ra Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Ra Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Ra Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Ra Lyons P., Marchonni L., Mashima J., Mazzarelli J., Mombaerts P., Ra Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Sasaki H., Soyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.,
                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";

Nature 409:685-690(2001).

-I-FUNCTION: Cooperates with TLR4 in the innate immune response to bacterial lipopolysaccharide (LPS), and with TLR2 in the response to cell wall components from Gram-positive and Gram-negative bacteria. Enhances TLR4-dependent activation of NF-kappa-B. Cells expressing both MD2 and TLR4, but not TLR4 alone, respond to LPS (By similarity).

-I-SUBUNIT: Heterogeneous homopolymer formed from homodimers; disulfide-linked. Belongs to the lipopolysaccharide (LPS) receptor, a multi-protein complex containing at least CD14, LY96 and TLR4. Binds to the extracellular domains of TLR2 and TLR4 (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20352025; PubMed=10891475; Rato K., Morrison A.M., Nakano T., Tashiro K., Honjo T.; Rato K., Morrison A.M., Nakano T., Tashiro K., Honjo T.; "ESOP-1, a secreted protein expressed in the hematopoietic, and reproductive systems of embryonic and adult mice."; Blood 96:362-364(2000).
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10-OCT-2003 (Rel. 42,
Lymphocyte antigen 96
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Akashi S., Shimazu R., Ogata H., N
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LY96 OR MD2 OR ESOP1
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similarity).
SUBCELIURAR LOCATION: Extracellular.
TISSUE SPECIFICITY: Highly expressed in such thymus, liver, kidney, ovary and decidua.
in testis, small intestine and skin.
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SEQUENCE
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat
Lymphocyte antigen 96 precursor (MD-2 prote
LY96 OR MD2 OR ESOPI.
                                            SEQUENCE FROM N.A., AND MUTAGENESIS OF CYS-95.

MEDILINE=21329172; PLDMed=11435474;

Schromm A.B., Lien E., Henneke P., Chow J.C., Yoshimura A., Hein Latz E., Monks B.G., Schwartz D.A., Miyake K., Golenbock D.T.;

Latz E., Monks B.G., Schwartz D.A., Miyake K., Golenbock D.T.;

"Molecular genetic analysis of an endotoxin nonresponder mutant line. A point mutation in a conserved region of MD-2 abolishes endotoxin-induced signaling ";

J. Exp. Med. 194:79-88 (2001).
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDILINE=20352025; PubMed=10891475;

Kato K., Morrison A.M., Nakano T., Tashiro K., Honjo T.;

Kato K., Morrison A.M., Nakano T., Tashiro K., Honjo T.;

"ESOP-1, a secreted protein expressed in the hematopoietic,
and reproductive systems of embryonic and adult mice.";

Blood 96:362-364(2000).
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InterPro; IPR0077110; Ig-like.
Pfam; PF02221; E1_DerP2_DerF2; 1.
smarr; SM00737; ML; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99288036; PubMed=10359581;
Shimazu R., Akashi S., Ogata H., Nagai Y., Fukudome K., Miyake K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MGD; MGI:1341909;
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EMBL; AK019283; BAB31645.1;
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ed. 189:1777-1782(1999)
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SEQUENCE FROM N.A

GO:0005886; GO:0015026; GO:0006961;

C:plasma membrane; TAS. F:coreceptor activity; TAS. P:antibacterial humoral res

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HGNC:17156; LY96

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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., William R., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RPCC. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                EMBL; AB018549; I
EMBL; AF168121; I
EMBL; BC020690; I
Genew; HGNC:1715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERACTION WITH TLR2 AND TLR4.

MEDLINE=21103214; PubMed=11160242;

Dziarski R., Wang Q., Miyake K., Kirschning C.J., Gupta Dziarski R., Wang L. Miyake T. (TLR2)-mediated responses "MD-2 enables Toll-like receptor 2 (TLR2)-mediated responses lipopolysaccharide and enhances TLR2-mediated responses Gram-positive and Gram-negative bacteria and their cell
                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Visintin A., Mazzoni A., Spitzer J.A., Segal D.M., "Secreted MD-2 is a large polymeric protein that efficiently lipopolysaccharide sensitivity to Toll-like receptor 4."; Proc. Natl. Acad. Sci. U.S.A. 98:12156-12161 (2001).
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; AAH20690.1;
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Q9KRB2;
16-OCT-2001
                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAIN-EI TOR N16961 / Serotype 01;

MEDLINE-20406833; PubMed-10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayyam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0007166; P:cell surface receptor linked signal transdu. .; GO:000668; P:cellular defense response; TAS. InterPro; IPR003172; El DerP2 DerP2. InterPro; IPR007110; II DerP2 DerP2. Ffam; PF02221; El DerP2 DerP2; 1. SMART; SM00737; ML; 1.
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28-FEB-2003 (Rel. 41, Last annotation update)
DNA topoisomerase I (EC 5.99.1.2) (Omega-protein)
(Untwisting enzyme) (Swivelase).
TOPA OR VC1730.
                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                         "DNA sequence cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                          Vibrio
                                                                                                                                               -
                                                                                                                                                                                        Nature 406:477-483(2000)
                        at one end o similarity: family.
                                     DNA, followed by passage and rejoining.
SUBUNIT: Monomer (By similarity).
MISCELLANEOUS: When a topoisomerase transiently breaks a D backbone bond, it simultaneously forms a protein-DNA link, which a tyrosyl oxygen in the enzyme is joined to a DNA ph at one end of the enzyme severed DNA strand.
SIMILARITY: Belongs to the prokaryotic type I/III topoisom
                                                                                                                                          FUNCTION: The reaction catalyzed by topoisomerases leads to the conversion of one topological isomer of DNA to another. CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 TISFSFKGIKFSKGKYKCVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 AGPVNNPEFTIPQGEYQVLLE
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                                                                                                                                                                                                                  of both chromosomes of the cholera pathogen Vibrio
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N-LINKED (GLCNAC...).
C-Y: ABOLISHES LPS-RESPONSE.
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                                        I/III topoisomerase
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R InterPro; IPR00380; DNA_tpisomrase.

R InterPro; IPR003601; DNATCDI_ATP_bind.

R InterPro; IPR003601; DNATCDI_ATP_bind.

R InterPro; IPR003601; DNATCDI_ATP_bind.

R InterPro; IPR006171; Toprim_dom.

R InterPro; IPR006171; Toprim_dom.

R InterPro; IPR006154; Toprim_dom.

R Pfam; PF011751; Toprim_I.

R Pfam; PF01751; Toprim; 1.

R Pfam; PF01751; Toprim; 1.

R Pfam; PF01396; ToP1Ac; 1.

R PRINTS; PR00417; PRTFISMRASEI.

R PRINTS; SM00437; TOP1Ac; 1.

R SMART; SM00436; TOPIBC; 1.

R SMART; SM00436; TOPRIM; 1.

R SMART; SM00436; TOPRIM; 1.

R SMART; SM00436; TOPRIM; 1.

R SMART; SM00436; TOPRIM; 1.

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                                                                                                                                                                                                                                                                                                                                        OB7SX6;

10-OCT-2003 (Rel. 42, Created)

10-OCT-2003 (Rel. 42, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)

10-OCT-2003 (Rel. 42, Last annotation update)

Adenylylsulfate kinase (EC 2.7.1.25) (APS kinase) (Adenosine-5'phosphosulfate kinase) (ATP adenosine-5'-phosphosulfate 3'-phosphotramsferase).

CYSC R VP0296.
STRAIN-RIMD 2210633 / Serotype O3:K6;
MEDLINE=22508454; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K.,
Iijima Y., Najima M., Nakano M., Yamashita A.,
Yasunaga T., Honda T., Shinagawa H., Hattori M.
"Genome sequence of Vibrio parahaemolyticus: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE004251; AAF94880.1; -. PIR; B82163; B82163.
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Vibrionaceae; Vibrio.
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TIGR; VC1730; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     641 INLGDEEGVINVLEEDVE----TAALRAKKRC-----PICETAMDAYLIDDKRK---LH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 LFLWTLIFPSCSGGGGGKAWPTHVV--CSDSGLEVLYQSCDPLQDFGFSVEKCSKQLKSN
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                                                                                                                                                                             FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VCG--NNPNCEGFIVEEGEFKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IVMTNILCPTCSRPMGIRTASTGVFLGCSGYGLP------PKERC----KTT
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717
327
876 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 695 C4
742 C4
327 DN
97909 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.0%; Score 78; DB
26.1%; Pred. No. 4.9;
                                                                                                                                                                                                                                                                                       Gammaproteobacteria; Vibrionales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C4-TYPE 1.
C4-TYPE 2.
DNA CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 4.9
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NA CLEAVAGE (BY SIMILARITY)
8A5BC9148CA1B753 CRC64;
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                                                                                     Yokoyama K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      There are no resi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40;
                        ., Uda T., Ta
, Kubota Y.,
M., Iida T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 876
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                                                               Kimura
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CCC - i - Fit
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Best Local S
Matches 50
                                                                                                                                                                                                                                                        CYSC VIBVU
Q8DE75;
10-OCT-2003
10-OCT-2003
                                                           STRAIN=CMCP6;
Rhee J.H., Kir
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lancet 361:743-749(2003)
-i- FUNCTION: Catalyzes the synthesis of activated
-i- CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phosphorylation; Complete proteome.

NP_BIND 39 46 ATP (BY SIMILARITY)

ACT_SITE 113 113 PHOSPHOSERINE INTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002891; APS_kinase.
Pfam; PF01583; APS_kinase; 1.
Transferase; Kinase; Cysteine biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AP005073; BAC58559.1; -.
HAMAP; MF_00065; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               distinct from that
                                                                                                                                                                                                                     10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ademylylsulfate kinase (EC 2.7.1.25) (APS kinase) (Adenosine-5'phosphosulfate kinase) (ATP adenosine-5'-phosphosulfate 3'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
   "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases:
-i- FUNCTION: Catalyzes the synthesis of activated sulfate:
-i- CATALYTIC ACTIVITY: ATP + adenylylsulfate = ADP + 3'
                                                                                                                                                   Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                              phosphotransferase).
                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                     NCBI_TaxID=672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphoadenylylsulfate.

PATHWAY: Sulfate activation; cysteine biosynthesis reductive branch; second step.

SIMILARITY: Belongs to the APS kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                            137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          125
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                                                                                                                                                                                 vulnificus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LC---SDLGFS----EQDRRENIR-RIGELAKLMADAGLIVLSAFISPHRAERQLVRD--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LMSQGSSV----LNFSYPICEAALPKFSFCGRRKGE-----QIYYAGPVNNPEFTIPQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KQFRAELKKQKPAVLW---FTGLSGAGKSTVAGALENRLAELGYHTYLLDGDN---VRHG
                                                                         Kim S.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of V. cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22894 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                            144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.9%;
26.3%;
                                                                         Chung S.S., Kim J.J., Moon
                                                                                                                                                                 Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 77;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHOSERINE INTERMEDIATE SIMILARITY).
; 03696F141F48199F CRC64;
                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                       207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 205;
                                                                                                                                                                   Vibrionales;
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                                                                           Ү.Н.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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)P + 3'-
                                                                         Jeong
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Best Local S
Matches 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGLD_HSVEA STANDARD; PRT; 402 AA P24872; (Rel. 21, Created) 01-MAR-1992 (Rel. 23, Last sequence update) 16-0CT-2001 (Rel. 40, Last annotation update) Glycoprotein D precursor (Glycoprotein T/)1 GD OR GP17/18 OR 72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphorylation; Complete proteome.

NP_BIND 39 46 ATP (BY SIMILARITY)
ACT_SITE 113 113 PHOSPHOSERINE INTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01583; APS kinase; 1.
ProDom; PD002350; APS kinase; 1.
TIGRPAMs; TIGR00455; apsK; 1.
Transferase; Kinase; Cysteine biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP; MF_00065; -; 1.
InterPro; IPR002891; APS_kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (Some send an email to license@isb-sib.ch).

    -!- SIMILARITY: Belongs to the APS kinase family.

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"Sequence analysis of the 4.7-kb BamHI-EcoRI herpesvirus type-1 short unique region."; Gene 101:203-208(1991).
-i- SIMILARITY: Belongs to the herpesviruses
                                                                                                                          [2]
SEQUENCE OF 242-402 FROM N.A.
MEDLINE=91276272; PubMed=1647359;
Halliburton I.W., Killington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Equine herpesvirus type 1 (strain AB1) (EHV-1).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSVEA
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                                                                                                        Elton D.M., Halliburton I.W.,
Bonass W.A.;
                                                                                                                                                                                                                                                                                                                               Bonass W.A.
                                                                                                                                                                                                                                                                                                                                                    Elton D.M.,
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=92268882; PubMed
Elton D.M., Halliburton
                                                                                                                                                                                                                                                                        "Identification of the equine herpesvirus type 1 gly as a homologue of herpes simplex virus glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphoadenylylsulfate.

PATHWAY: Sulfate activation; cysteine biosynthesis reductive branch; second step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139
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                                                                                                                                                                                                                                              mologue of herpes simplex virus
Virol. 73:1227-1233(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -TQDRRENIR-RIGELAKLMADAGLIVLTAFISPHRAERQLVRD--LLPEGEFIEVFVNT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LWILLFPSCSGGG------GGKAWPTHVVCSDSGLEVLYQSCDPLQDFGFSVEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LW---FTGLSGAGKSTVAGALENRLAEQGFHTYLLDGDN---VRHGLC---SDLGFS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYPICEAALPKFSFCGRRKGEQIYYAG-----PVNNPEFTIPQGE--YQVLLELYTEK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                 PubMed=1316942;
burton I.W., Killington R.A., Meredith D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22886 MW;
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25.0%;
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Pred. No. 1.1;
26; Mismatches
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                                                                                 fragment
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ein D.";
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glycoprotein

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RESULT
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Best Local Similarity
Matches 44; Conserv
  aquine herpesvirus t
glycoproteins with hon
gE.";
J. Gen
VGLD HSVEB
P24379;
01-MAR-1992
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CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
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TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Glycoprotein D precursor (Glycoprotein 17/18)
GD OR GP17/18 OR 72.
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                                                                                                                                                                                                                MEDLINE=92295566; PubMed=1318606;
Telford E.A.R., Watson M.S., McBride
"The DNA sequence of equine herpesvir
                                                                                                                                                                                                                                                                                                                                                                 Equine herpesvirus type 1 (strain Ab4p) (EHV-1), and Equine herpesvirus type 1 (strain Kentucky D) (EHV-1 Viruses, aBDNA viruses, da RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSVEB
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SIGNAL
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                                                                                                                                                                                            Virology
                                                                                                                                                                                                                                                                                    STRAIN-AB4P;
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Pro; IPR007110; Ig-like.
PF01537; Herpes_glycop_D; 1.
protein; Transmembrane; Signal.
L 30 POTENTIAL.
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ce of equine herpesvirus-1.";
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL)
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-LINKED (GLCNAC. . .) (POTENTIAL).
-LINKED (GLCNAC. . .) (POTENTIAL).
-LINKED (GLCNAC. . .) (POTENTIAL).
78A0593232D0238C CRC64;
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No. 2
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                                               \vdash
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Best Local S
Matches 44
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InterPro; IPRO02896; Jerpes_blycop_D; 1.

Pfam; PP01537; Herpes_glycop_D; 1.

Pfam; PP01537; Herpes_glycop_D; 1.

Pfam; PP01537; Herpes_glycop_D; 1.

POTENTIAL.

1 19 POTENTIAL.

SIGNAL 1 19 POTENTIAL.

POTENTIAL.

CHAIN 20 452 EXTRACELIULAR (POTENTIAL).

TRANSMEM 406 422 POTENTIAL).

TRANSMEM 406 422 CYTOPLASMIC (POTENTIAL).

TRANSMEM 423 452 CYTOPLASMIC (POTENTIAL).

CARBOHYD 103 103 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 111 111 N-LINKED (GLCNAC. .) (POTENTIAL).

CARBOHYD 396 396 N-LINKED GLCNAC. .) (POTENTIAL).

CARBOHYD 396 396 N-LINKED GLCNAC. .) (POTENTIAL).

SEQUENCE 452 AA; 51099 MW; CF51E914F7F2E9DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MURG_CAMJE STANDARD; PRT; 342 AA.

09PN02;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide)
pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
pyrophosphoryl-undecaprenyl-PP-MurNAc-pentapeptide-UDPG1cNAc GlcNAc
STRAIN=NCTC 11168;

MEDLINB=20150912; PubMed=10688204;

Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,

Parkhill J., Wren B.W., Mungall K., Feltwell T., Holroyd S.,

Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,

Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,

Whitehead S., Barrell B.G.;

Whitehead S., Barrell B.G.;

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PIR; I36802; VGBEG3.
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                                                                                                                                                                                                                                                                                                                                                                 Campylobacter jejuni.
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Campylobacteraceae; Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transferase)
                                                                                                                                                                                                                                                                                   SEQUENCE
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44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKSNINIREGII--LREDIKELELDLALMSQGSSVL------NFSYPICEAA 105
                                                                                                                                                                                                                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CPIAFEQNFGNPDRCKTPEQYSRGEVFTRRFLGEFNFPQGEHMTWLKFW 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LP----KFSFCGRRKGEQIYYAGPVNN----PEFTIPQGEYQVLLELY 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -RSDILWQASLITMAAETDDELGLVLAAPAHSASGLYRRVIEIDGRRIYTDFSVTIPSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGFTATLFLWTLIFPSCSGGGGGKAWPTHVVCSDSGLEVLYQSCDPLQDFGFSVEKCSKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Belongs to the herpesviruses glycoprotein D is uncertain whether Met-1 or Met-51 is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.9%;
26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 76.5; DB
Pred. No. 3.1;
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
(POTENTIAL)
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L outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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RAAR RAAR
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RPOB_CLOAB
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Best Local S
Matches 37
                                                                                                                                                                                                                                   RPOB CLOAB

Q97EG9;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.

Corpa Chain) (RNA polymerase beta subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAMAP; MF 00033; -; 1.

HAMAP; MF 00033; -; 1.

InterPro; IPR007235; Glyco_trans_28_C.

InterPro; IPR004276; Glyco_trans=28.

InterPro; IPR0064276; MurG.

Pfam; PF04101; Glyco_trans_28_C; 1.

Pfam; PF04101; Glyco_trans_28_C; 1.

Pfam; PF03033; Glyco_trans_28_C; 1.

TIGRPAMs; TIGR01133; murG; I.

Transferase; Glycosyltransferase; Cell division; Cell wall; Membrane;

Inner membrane; Peptidoglycan synthesis; Complete proteome.

SEQUENCE 342 AA; 38683 MW; F7013138706889E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE FROM N.A.
STRAINSATCC 824 / DSM 792 / VKM B-1787;
MEDLINE=21359325 , PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V.,
Gibson R., Lee H.M., Dubois J., Qiu D., H
Tatusov R.L., Sabathe F., Doucette-Stamm
Bennett G.N., Koonin B.V., Smith D.R.;
                                                                                                                                                                                                          Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia;
Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL139077; CAB73295.1; -. PIR; D81306; D81306.
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                                                                                                                                                                               NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Cell wall formation. Catalyzes the transfer of a GlCN7 subunit on undecaprenyl-pyrophosphoryl-MurNAc-pentapeptide (lipid intermediate I) to form undecaprenyl-pyrophosphoryl-MurNAc-(pentapeptide)GlCNAc (lipid intermediate II) (By similarity). CATALYTIC ACTIVITY: UDP-N-acetylglucosamine + Mur2Ac(oyl-L-Alagama-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol = UDP + GlCNAc-(1-4)-Mur2Ac(oyl-L-Ala-gamma-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol.

GlUNAc-(1-4)-Mur2Ac(oyl-L-Ala-gamma-D-Glu-L-Lys-D-Ala-D-Ala)-diphosphoundecaprenol.

SUMILARITY: Beptidoglycan biosynthesis; last step.

SUMCELLULAR LOCATION: Inner membrane-associated (By similarity).

SIMILARITY: Belongs to the glycosyltransferase family 28. MurG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LDEF----FKSILKLNLENIST 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEELILOGEAOATTETALEKKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGASTL---FELCANTLETIFIFYPYAAKNHQYFNAKFLQDQALC----QIFMQNSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQNIKITHO-CGK-NDF----EKCKKHYQS-LNIQADIFDFSLNLEEKMKN--ADLAISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.8%;
ilarity 25.7%;
Conservative 2
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                                                                                                                                                                                                                                Clostridiales;
                        , Makarova K.S.,
Hitti J., Wolf
m L., Soucaille
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P.
                                              Zeng
Y.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
                          Daly M.J.
                                                                    Ö
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(lipid
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Eukaryota; Metazoa; (
Mammalia; Eutheria; F
NCBI_TaxID=9606;
[1]

Primates; Chordata;

Catarrhini; Hominidae;

Craniata; Vertebrata; Euteleostomi;

Homo sapiens

(Human)

UDP-N-acetylhexosamine pyrophosphorylase (Antigen X) (AGX) (Speassociated antigen 2) [Includes: UDP-N-acetylgalactosamine pyrophosphorylase (EC 2.7.7.-) (AGX-1); UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23) (AGX-2)].

update)

A

UAP1_HUMAN STANDARD; PRT; 522 AA Q16222; 15-JUL-1999 (Rel. 38, Created) 15-JUL-1999 (Rel. 38, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation updat

NAMDH

δ

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RESULT 15
UAP1_MPNA
ID 1—UAP1
AC Q1622
AC Q1622
AC Q1622
DT 15-U
DT 15-U
DT 15-W
DE Assoc
DE Pyroj
DE Pyroj
GN UAP1
OS Homo
OC Euka
OC NCBI
RN [1]
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InterPro; IPR007644; RNA pol Rpb2 1.

InterPro; IPR007642; RNA pol Rpb2 2.

InterPro; IPR007643; RNA pol Rpb2 3.

IN InterPro; IPR007641; RNA pol Rpb2 7.

IN InterPro; IPR007120; RNA pol Rpb2 7.

IN Pfam; PF04563; RNA pol Rpb2 1; 1

IN Pfam; PF04565; RNA pol Rpb2 3; 1.

IN Pfam; PF04565; RNA pol Rpb2 3; 1.

IN Pfam; PF04560; RNA pol Rpb2 3; 1.

IN Pfam; PF04560; RNA pol Rpb2 3; 1.

IN Pfam; PF04560; RNA pol Rpb2 3; 1.

IN Pfam; PF04560; RNA pol Rpb2 7; 1.

IN Pfam; PF04560; RNA pol Rpb2 7; 1.

IN Pfam; PF04560; RNA pol Rpb2 7; 1.

IN Pfam; PF04560; RNA pol Rpb2 7; 1.

IN PGNSITE; PS01166; RNA POL RPBTA; 1.

IN PACSITE; PS01166; RNA POL BETA;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE007809; AAK81081.1; -. PIR; F97286; F97286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence and comparative analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriol. 183:4823-4838(2001).
- FUNCTION: DNA-dependent RNA polymerase cataly.
of DNA into RNA using the four ribonucleoside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tities requires a license agreement (S send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               substrates.
CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enzyme which is composed of 2 alpha chains, 1 beta chain, an beta' chain.
SIMILARITY: Belongs to the RNA polymerase beta chain family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {RNA}(N).
SUBUNIT: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRE--DIK--ELFL-DLALMS-QGSSVLNFSYPICEAALPK----FSFCGRRKGEQIYY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATVIPN-----RGAW---LEYETDSNSVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGPVNNPEFTIPQGEYQVLLELYTEKRSTV 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NKETGEVKEQEVFMGDFPLMTEQGTFIINGAERVIVSQLVRSPGAYYDYIVDKNGKKLFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNGLQEIFDDINPIQDYTGNLILEFIGYKLDMDNIKYSVEECKERDTTYAAPLKVKVRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium acetobutylicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enzyme consists of the is composed of 2 alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.8%; Score 75.5;
19.3%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sigma chain and chains, 1 beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1241;
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SEQUENCE FROM N.A. (ISOFORMS ISSUE=Testis;

AGX1

AND

AGX2)

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RY MEDLINE-9843844; PubMed-9765219;
RX MEDLINE-98438464; PubMed-9765219;
RA Wang-Gillam A., Pastuszak I., Elbein A.D.;
RA Wang-Gillam A., Pastuszak I., Elbein A.D.;
RT Mang-Gillam A., Pastuszak I., Elbein M.D.
CC of UTP. AGXI converts GalNaC-1-P into UDP-GalNac in the presence of UTP.
CC of UTP, AGXI converts GalNaC-1-P into UDP-GalNac Inthe presence of UTP.
CC of UTP, AGXI converts GalNaC-1-P into UDP-GalNac Inthe presence of UTP.
CC of UTP, AGXI converts GalNaC-1-P into UDP-GalNac Inthe presence of UTP.
CC of UTP, AGXI converts GalNaC-1-P into UDP-GalNac Inthe presence of UTP.
CC of UTP, AGXI converts GalNaC-1-P into UDP-GalNac Inthe UDP-GalNac Inthe UTP-GalNac Inthe UTP-
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EMBL; AB011004; BAA31202.1; -.
PDB; 1JV1; 28-AUG-02.
PDB; 1JV3; 28-AUG-02.
PDB; 1JVD; 29-AUG-02.
PDB; 1JVC; 30-AUG-02.
PDB; 1JVC; 30-AUG-02.
PDB; 1JVC; 30-AUG-02.
PDB; 1JVC; 30-AUG-02.
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"The eukaryotic UDP-N-acetylglucosamine pyrophosphorylases:
cloning, protein expression, and catalytic mechanism.";
J. Biol. Chem. 273:14392-14397(1998).
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Diekman A.B., Goldberg E.;
"Characterization of a human antigen with sera from infertile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew, HGNC:12457, UAP1.

MIM; 602862; ---
GO; GO:0003977; F:UDP-N-acetylglucosamine diphosphorylase act. ..;
GO; GO:0005048; P:UDP-N-acetylglucosamine biosynthesis; TAS.
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                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002618; UDPGP.
Pfam; PF01704; UDPGP; 1.
Transferase; Nucleotidyltransferase; Antigen; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                Polymorphism; 3D-structure.
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IsoId=016222-1; Sequence=Displayed;
Name=AGX1; Synonyms=AGX-1;
IsoId=016222-2; Sequence=VSP_004483;
IsoId=016222-2; Sequence=VSP_004483;
TISOIDE SPECIFICITY: Widely expressed. AGX1 is more abundant in testis than AGX2, while AGX2 is more abundant than AGX1 in somatic tissue. Expressed at low level in placenta, muscle and liver. DISEASE: ANTIGEN IMPLICATED IN ANTIBODY-MEDIATED MALE INFERTILITY.
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470
POTENTIAL.
POTENTIAL.
Missing (in isoform AGX1).
/FTId=VSP_004483.
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301 VVEYSEISLATAQKRSS--
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                                                                                                      28;
                                                                                                                 Similarity
                   -IKELFLDLALMSQGSSVLNFSYPICEAALPKFSFCGRRKGEQIYYAGPVNNPBETIP 134
                                                WSTHVYCVDN---ILVKVADP-RFIGFCIQKGADCGAKVVEKTNPTBPVGVVCRVDGVYQ 300
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522 AA;
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                                                                                                                                                                                              418
                                                                                                                8.7%;
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                                                                                                     19; Mismatches
                                                                                                                Score 75; DB 1; Length 522; Pred. No. 5.4;
                                                                                                                                                      P -> H (in dbSNP:1128539).
/FTId=VAR_014935.
MISSING (IN REF. 1).
; C823A9AD8659A135 CRC64;
                                                                                                      35;
 ----DGRLLFNAGNIANHFFTVP 336
                                                                                                      Indels
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Search completed: April 29, 2004, 15:24:51 Job time : 18 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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1: sp_archea:*
2: sp_bacteria:*
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 Q8miq1 oryctolagus
O821196 arabidopsis
Q7tum5 prochloroco
Q91193 arabidopsis
O58069 pyrococcus
Q9sin9 arabidopsis
Q9vsu2 drosophila
Q1213 saccharomyc
Q9606 drosophila
Q1213 saccharomyc
Q9606 drosophila
Q9uy77 pyrococcus
Q22by9 yersinia pe
Q76660 toxoplasma
Q71227 fugu rubrip
Q9m994 arabidopsis
Q8rvq6 arabidopsis
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       AIAGSAEEMIFCLNFTII 154
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Q29113 sus scrota	snewanel		Q8d173 yersinia pe	drosophila	ric	r3 mus	rat	0	w	caen	Q9ttw0 bos taurus	Yzo C	aenorhabo	Q9x196 arabidopsis	Q96gm2 homo sapien	046493 bos taurus	P93750 arabidopsis	Q8rwh6 arabidopsis	Q8gx23 arabidopsis	Q8w4y5 lycopersico	Q81j48 bacillus ce	Q81vt8 bacillus an	arak	Q23653 caenorhabdi	1d7 oryza i	245 equine	Q20250 caenorhabdi	Q94ai6 arabidopsis

ALIGNMENTS

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SEQUENCE FROM N.A.

Kajikawa O., Frevert C.W., Martin T.R.;

Kajikawa O., Frevert C.W., Martin T.R.;

"Molecular cloning of rabbit MD-2.";

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AY101395; AAM50061.1; -.

EMBL; AY101395; AAM50061.1; -.

EMBL; IFR003172; B1 DerP2_DerF2.

InterPro; IFR003172; B1 DerP2_DerF2.

InterPro; IFR003173; MI; 1.

EMART; SM00737; ML; 1.

EMART; SM00737; ML; 1.

EMART; SM00737; ML; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                           30 HVVCSDSGLEVLYQSCDPLQ-DFGFSVBKCSKQLKSNINIRFGIILREDIKELFLDLALM 88
                                                                                                                                                                                                                                                                                                   n 13.3%; Score 115; DB 6; Similarity 25.4%; Pred. No. 0.00027;
                                                                                                                             HWYCKSADATYSYTYCDNMEIPISINVEPCITLKGTQGLLHIFYIPRRDMNQLYLNLYI- 80
                                                             SQGSSYLNFSYP----ICEAALPKFSFCGRRKGEQIYYAGPVNNPEFTIFQGEYQVLLE 143
----SVNSMDLPKRKEIICKGSDDVYSFCRALKGETVNTTVPFSFKGIRLSKGQYRCVVB
                                                                                                                                                                                                                                                                                                                                                                                                           160 AA; 18186 MW; A2C1E0B46E762F43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                      Conservative
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RESULT 2
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Copia-like retroelement p
ATZG19840
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 Q7TUM5;
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Q1-OCT-2003
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Freuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AC005169; AAC62132.1; -, p1R; G84581; G84581.
G0; G0:0003677; F:DNA binding; IEA.
G0; G0:0003610; P:DNA recombination; IEA.
InterPro; IPR001584; Rve.
InterPro; IPR001584; Znf_CCHC.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00939; C2HCZNFINGER.
SMART; SM00343; ZNF_C2HC; 1.
PROSITE; PS50158; ZF_CCHC; 1.
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Pfam; PF00098; zf-CCHC; 1.
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STRAIN=cv. Columbia;
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                            R InterPro; IPRO02885; PPR.
R InterPro; IPR002885; PPR.
R InterPro; IPR008941; TPR-like.
Pfam; PF01535; PPR; 25.
TIGRPAMs; TIGR00756; PPR; 24.
SEQUENCE 1440 AA.
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Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,
Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,
Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
Webb E.A., Zinser E.R., Chisholm S.W.,
"Genome divergence in two Prochlorococcus ecotypes reflects oceanic
niche differentiation.";
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Q9LV30;
01-OCT-2000
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Submitted (
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EMBL; BX572100; CAE22042.1; -.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis
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SEQUENCE 204 AA; 22142 MW;
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                                                                                                                                                                                      Nakamura Y.;
"Structural analysis of Arabidopsis Sequence features of the regions of TAC and BAC clones.";
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                     Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ofituku Y. Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi Aski K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.; Robb F.T., Horikoshi K., "Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.";
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   Eukaryota;
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   Viridiplantae;
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45912 MW;
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Streptophyta;
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Pred. No. 3.8;
27; Mismatches
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2; Mismatches
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694855F337C5DD8D CRC64;
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   Embryophyta;
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PIR; H84723; H84723.

GO; GO:0003824; F:catalytic activity; IEA.

GO; GO:0004806; F:triacylglycerol lipase acti
GO; GO:0006629; P:lipid metabolism; IEA.

InterPro; IPR0003921; Lipase_3.

InterPro; IPR000379; Ser_estre.

Pfam; PF01764; Lipase_3; 1.

SEQUENCE 484 AA; 54923 MW; 74650CD21BB78:
                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update
01-OCT-2003 (TrEMBLrel. 25, Last annotation upda
CG4821 protein.
TEQUILA OR CG4821 OR CG4948 OR CG18403.
Drosophila melanogaster (Fruit fly.)
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insect
Neoptera; Endopterygota; Diptera; Brachycera; Mu
Ephydroidea; Drosophilldae; Drosophila.
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STRAIN=20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.J.
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Salzberg S.L., Fraser C.M., Venter J.C.;
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Q9VSU2; Q9VSU1;
01-MAY-2000 (TrE
01-OCT-2002 (TrE
STRAIN-Berkeley;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G
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T.B.,
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RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ra Ballew R.M., Basu A., Barwendale J., Bayraktaroglu L., Beasley E.M., Ra Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I., Ra Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ra Dudbon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P. Ra Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Pleischmann W. Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Alashi M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A. Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Ra Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Walson D.L., Ra Ra Reinert K., Remington K.S., Saunders R.D.C., Scheeler F., Shen H., Ra Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Sahth T., Ra Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Sahth T., Ra Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Sahth T., Ra Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Sahth T., Ra Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Sahth T., Ra Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Sahth T., Ra Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Sahth T., Ra Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Sahth T., Ra Shue B.C., Scheeler F., Zaveri J.S., Zhan M., Zhang S., Yao Q.A., Zheng L., Yeh R.-F., Zaveri J.S., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O. Rhu J., Shuh G., Shuh J., Shuh G.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

RA Balzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,

RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

RA Carlson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,

RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

RA Ibegwam C., Jalaii M., Kruse D., Li P., Mattei B., Moshrefi A.,

RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,

RA Pacleb J., Paragas V., Park S., Patel S., Pfeifer B.,

RA Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

RA Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,

RI "Sequencing of Drosophila melanogaster genome.",

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
INTERPRETATION (NEEP-2002) to the E I SIMILARITY: BELONGS TO PE EMBL; AE003553; AAF50319.3; -HSSP; P00750; IRTF. FlyBase; FBgn0023479; Tequila GO; GO:0005576; C:extracellul
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                                                                                                                                                                                                                  FlyBase;
Submitted (SEP-2002)
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GO; GO:0005524; F:ATF binding; IEA.
GO; GO:0005524; F:Chymotrypsin activity; IEA.
GO; GO:0008613; F:chymotrypsin activity; IEA.
GO; GO:0004283; F:chymotrypsin activity; IEA.
GO; GO:0005044; F:scavenger receptor activit
GO; GO:0005042; F:trypsin activity; IEA.
GO; GO:0006030; P:proteolysis and peptidoly;
GO; GO:0006030; P:proteolysis and peptidoly;
GO; GO:0005031; P:proteolysis and peptidoly;
GO; GO:0015992; P:proteolysis and peptidoly;
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InterPro; IPR001314; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR00139; SrCR; 2.
Pfam; PF00050; IDLA; 2.
Pfam; PF00050; IDLA; 2.
Pfam; PF00050; IDLA; 2.
SMART; SM00102; STCR; 2.
PFANGITE; PS00120; STCR; 2.
PROSITE; PS00120; STCR; 2.
PROSITE; PS00135; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN DOM; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
PROSITE; PS00134; TRYPSIN SER; 1.
PROSITE; PS00135; TRYPSIN SER; 1.
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Q12139;
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Q12030;
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Q1-UNOV-1996 (TremBirel. 24, La
Q1-UN-2003 (TremBirel. 24, La
                          STRAIN=AB972;
Badcock K., Bowman S.
Walsh S.V., Barrell I
Submitted (APR-1996)
                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                               (APR-1996)
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i; F:AITP binding; IEA.
i; F:chitin binding; IEA.
j; F:chymotrypsin activity; IEA.
j; F:peptidase activity; IEA.
d; F:scavenger receptor activity.
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                                                          Pearson
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Al Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
A Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
A Nunco J., Pacleb J., Paragas V., Park S., Photanenavong S., Wan K.,
A Vu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (ANG-2001) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

REMBL; AY052072; AAK93496.1; --
REMBL; AY052072; AAK93496.1; --
REMBL; AY052072; AAK93496.1; --
REMBL; AY052072; AAK93496.1; --
REMBL; AY052072; AAK93496.1; --
REMBL; AY052072; AAK93496.1; --
REMBL; AY052072; AAK93496.1; --
REMBL; AY052072; C:extracellular; IEA.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005576; F:hitin binding; IEA.
GO; GO:0004263; F:chitin binding; IEA.
GO; GO:0004263; F:cpaptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0004030; P:chitin metabolism; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
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Best Local Similarity
Matches 37; Conserv
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Q960G6;
01-DEC-2001
01-DEC-2001
01-CCT-2003
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SGD;
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PROSITE; PS00128; ZINC_FINGER C2H2_1; 1.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.

Hypothetical protein; Metal-binding; Zinc; Zinc-finger.

SEQUENCE 1133 AA; 130116 MW; 77F6F3C9E3760DAA CRC64;
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EMBL; Z49274; CAA89276.1; -.
PIR; S54496; S54496.
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Badcock K., Churcher
Submitted (MAY-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TEQUILA OR CG4821 OR CG4948 OR CG18403.
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barrell B., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 DPLQDFGFSVEKCS---------KQLKS---NINIRFGII----LREDIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFQPPSKTYIIQSLLLVEGY-EKTST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 25, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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to the EMBL/GenBank/DDBJ databases
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Pred. No.
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R PRINTS; PRO07261; LDLRECEPFOR.

R PRINTS; PRO0258; SPERACTRCPTR.

R SMART; SM00494; ChtBJ2; 10.

R SMART; SM00192; LDLa; 2.

R SMART; SM00192; Tryp_SPc; 1.

R SMART; SM00192; Tryp_SPc; 1.

R PROSITE; PS00152; ATPASE ALPHA_BETA; 1.

R PROSITE; PS00152; ATPASE ALPHA_BETA; 1.

R PROSITE; PS00166; LDLRA_1; 1.

R PROSITE; PS00166; LDLRA_1; 2.

R PROSITE; PS00420; SRCR_1; 2.

R PROSITE; PS00420; SRCR_1; 2.

R PROSITE; PS00240; TRYPSIN_DOM; 1.

R PROSITE; PS00134; TRYPSIN_SER; 1.

R PROSITE; PS00134; TRYPSIN_SER; 1.

R PROSITE; PS00135; TRYPSIN_SER; 1.

R PROSITE; PS00135; TRYPSIN_SER; 1.

R PROSITE; PS00135; TRYPSIN_SER; 1.
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Best Local (
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InterPro; IPR009003; Cyg_Ser_trypsin.
InterPro; IPR002172; LDL_receptor A.
InterPro; IPR001254; Peptidase_S1A.
InterPro; IPR001214; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR00190; Sror_receptor.
Pfam; PF001607; CBM_14; 10.
Pfam; PF00057; ldl_recept_a; 2.
Pfam; PF00057; ldl_recept_a; 2.
Pfam; PF00058; SRCR; 2.
Pfam; PF00058; SrorRyPSIN.
PRINTS; PR00258; SPERACTROPTR.
PRINTS; PR00258; SPERACTROPTR.
PRINTS; PR00258; SPERACTROPTR.
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OSUY77
OSUY77,
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OL-MAY-2000 (TrEMBLrel. 13, Created)
OL-MAY-2000 (TrEMBLrel. 13, Last sequence
OL-JUN-2003 (TrEMBLrel. 24, Last annotatic
ORDY related from CALDICELLULOSIRUPTOR SA(
TRANSPAY TELATOR TRANSPAY
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SEQUENCE
                                                                                                                                             SEQUENCE FROM N.A. STRAIN=GE5 / Orsay;
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Pyrococcus abyssi.
Archaea; Euryarchaeota;
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InterPro; IPR002557; Chitin_bind_PerA.
InterPro; IPR009035; Cys_Ser_bind_PerA.
InterPro; IPR009003; Cys_Control
InterPro; IPR00900179; INT_recontrol
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                                                                         Pfam; PF01882; DUF58; 1.
                                                                                                                                                                                                                                                                                                                                                                Heilig R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CBI_TaxID=29292;
                                                                                                               nterPro; IPR002881; DUF58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 TMILSACPDGTNGLHLYPYDAGKYVRCSDGG-KMSIQSCENQMAFSLSQRACRPSRLVST
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44831 MW;
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tation update)
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Query Match
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Conservative

9.0%; Score 77.5; D)
23.4%; Pred. No. 8.7;
cive 31; Mismatches

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InterPro; IPR001480; Blectin.
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InterPro; IPR000858; Slocus_glycop.
Pfam; PF01453; Agglutinin; I.
Pfam; PF00954; S locus_glycop; 1.
SMART; SM00108; B_lectin; 1.
SMART; SM00473; PAN_AP; 1.
                                                                          Q8ZBY9;
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01-JUN-2003
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SEQUENCE
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Kusaba M., Nishio T., Satta Y., Hinata K., Ockendon D.;
Kusaba M., Nishio T., Satta Y., Hinata K., Ockendon D.;
"Striking sequence similarity in inter- and intra-specific of class I SLG alleles from Brassica oleracea and Brassica campestris: Implications for the evolution and recognition mechanism.";
Proc. Natl. Acad. Sci. U.S.A. 94:7673-7678(1997).
EMBL; D85205; BAA21939.1; -.
EMBL; T14529.
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Brassica oleracea (Cauliflower).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Eukaryota; Magnoliophyta; eudicotyledons; core eu

Spermatophyta; Magnoliophyta; eucicateae; Brassica.

eurosids II; Brassicales; Brassicaceae; Brassica.
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                  Putative exported YPO3241.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27;
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                                                                                                                                                                                                                                                                                                                                             FYLL--KSGFQVHRSGPWNGVRFSGIPENQKLSYMVYNFTENSEEVA 246
                                                                                                                                                                                                                                                                                                                                                                                        FSFCGRRKGEQIYYAGPVNNPEFT-IPQGE-YQVLLELYTEKRSTVA 153
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xported protein.
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428 AA; 48724 MW; 18E04542C7293BEA CRC64;
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                                                                                                                                                                                             PRELIMINARY;
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                                                                          Created)
Last sequence update)
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X MEDLINE=21470413; PubMed=11586360;

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Aparkhill J., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

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Matches 37
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076660;
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01-NOV-1998
01-CCT-2003
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EMBL; AF078678; AAC27649.1; -.
Interfro; IPR007226; SAG.
Pfam; PF04092; SAG; 1.
PRINTS; PR01801; SURFCEANTIGN.
SEQUENCE 396 AA; 42105 MW; 7E96A39F44D15A0
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Eukaryota; Alveolata;
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Hehl A., Boothroyd J.C.;
"SRS4, a member of the SAG1 family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRS4.
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                                                                                                                                                                              l Similarity 21.1
37; Conservative
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GEEWTLQLQESDLPLTDKAFFVGCDNKAGAGKDVQTSSKECKVDFNVKARPSFVAENNVV
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Pred. No. 10;
22; Mismatches
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SEQUENCE
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STRAIN-CV. columbia;

SITAIN-CV. columbia;

Liu S., Yu G., Lee J., Sakano H., Jhaveri A., Lenz C., Toriumi M.,

Chin S., Chiou J., Choi E., Gonzalez A., Howng B., Koo T., Li J.,

Liu A., Pham P., Vaysberg M., Altafi H., Buehler E., Chao Q., Conn L.,

Conway A.B., Hansen N., Johnson-Hopson C., Khan S., Kim C., Lam B.,

Nguyen M., Palm C., Shinn P., Tambunga G., Davis R., Ecker J.,

Pederspiel N., Theologis A.;

"The sequence of BAC F14023 from Arabidopsis thaliana chromosome 1.";

"The sequence of BAC F14023 from Arabidopsis thaliana chromosome 1.";
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Jones A.K., Elgar G., Sattelle D.B.;
"The nicotinic acetylcholine recepto:
Fugu rubripes.";
Genomics 0:0-0(2003).
EMBL; AY299468; AAP58383.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=31033;
    Theologis A.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases EMBL; AC012654; AAF43235.1; -.
                                                                                                                                        SEQUENCE FROM N.A. STRAIN=cv. columbia;
                                                                                                                                                                                                                                                                            Submitted (NOV-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 GRVTWTPPALYCSSCGVKVEY-----FPFDWQNCSMQFRSYTYDSTEIDVQYALNIR 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 -EDIKELFLDLALMSQG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGKAW-PTHVVCSDSGLEVLYQSCDPLQDFGFSVEKCSKQLKS-----NINIRFGIILR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQEIRÉIQLDEAFTEGG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 480 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55233 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.9%; Score 77; DB 13; Length 480; 29.9%; Pred. No. 13;
                                                                                                                                                                                                                                                                  F14023 from Arabidopsis thaliana chromosome 1."; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor gene family of the pufferfish,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D0CD2322938E06C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             739 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
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Best Local Similarity
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SEQUENCE 739 AA;
299
                         105 ALPKFSFCGRRKGEQIYYAGPVNNPEFTIPQGEYQVLLELYTEK 148
                                                      264 VÓGKGYK-DKCYEÓIRKAVEDRÉNRLLTLVFEDLK-----
                                                                                48 LODFGFSVEKCSKOLKSNINIRFGIILR---EDIKELFLDLALMSQGSSVLNFSYPICEA 104
                                                                                                             25;
ALEEARMIGEELGDIYDYVAPCFPPRYEI----FQLMVNLYTER
                                                                                                             8.9%; Score 77; DB milarity 24.0%; Pred. No. 21; Conservative 17; Mismatches
                                                                                                                                                                      84156 MW;
                                                                                                                                                                      9EDASEEEF888BAEB CRC64;
                                                                                                                               DB 10; Length 739; 21;
                                                                                                                30;
                                                                                                                Indels
 338
                                                                                                                32;
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                                                           298
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Search completed: April 29, 2004, 15:23:13
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